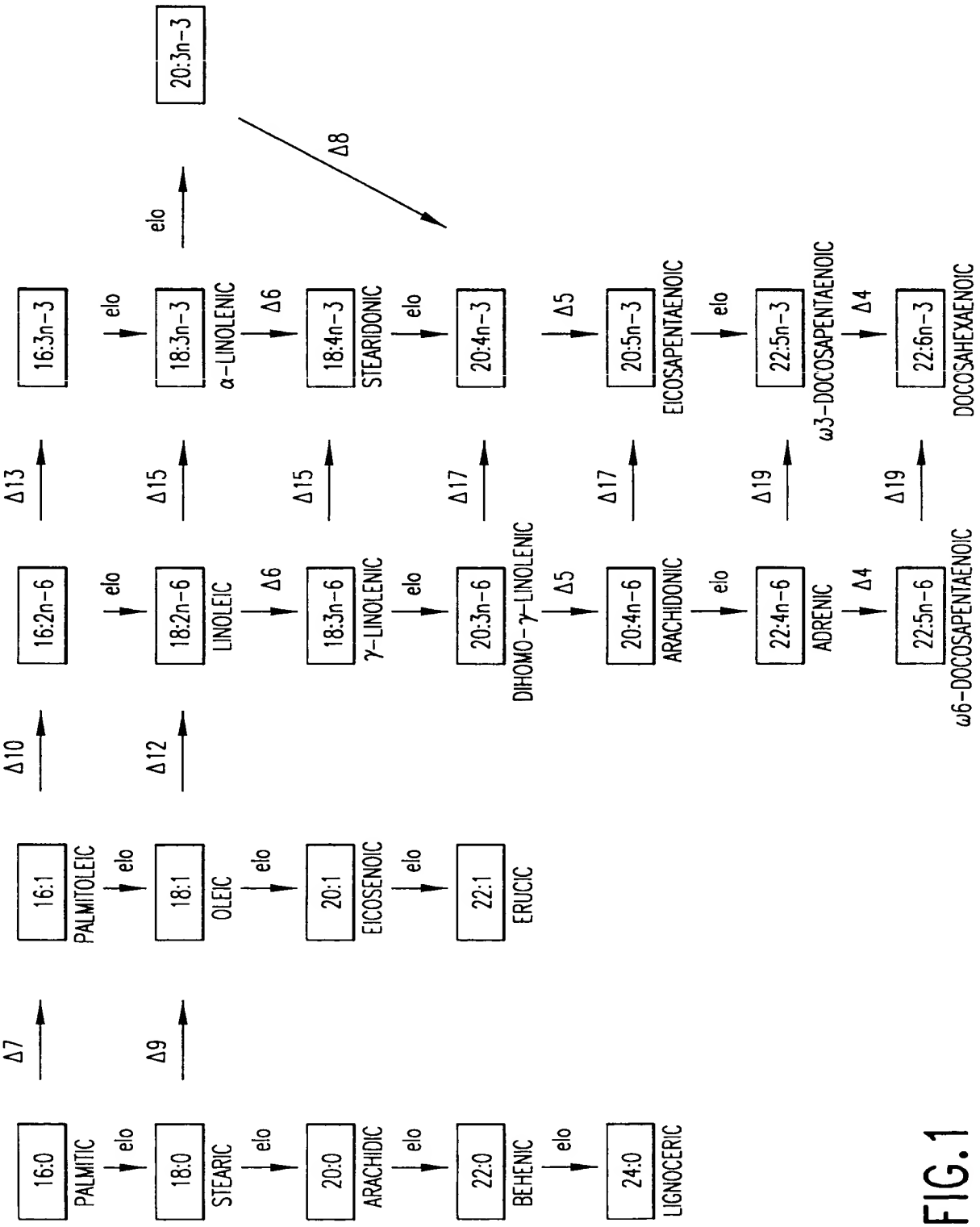
16:0
PALMITIC
elo
18:0
STEARIC
elo
20:0
ARACHIDIC
elo
22:0
BEHENIC
elo
24:0
LIGNOCERIC
Δ7
Δ9
16:1
PALMITOLEIC
elo
18:1
OLEIC
elo
20:1
EICOSENOIC
elo
22:1
ERUCIC
Δ10
Δ12
16:2n-6
elo
18:2n-6
LINOLEIC
Δ6
18:3n-6
γ-LINOLENIC
elo
20:3n-6
DIHOMO-γ-LINOLENIC
Δ5
20:4n-6
ARACHIDONIC
elo
22:4n-6
ADRENIC
Δ4
22:5n-6
ω6-DOCOSAPENTAENOIC
Δ13
Δ15
Δ15
Δ17
Δ17
Δ19
Δ19
16:3n-3
elo
18:3n-3
α-LINOLENIC
Δ6
18:4n-3
STEARIDONIC
elo
20:4n-3
Δ5
20:5n-3
EICOSAPENTAENOIC
elo
22:5n-3
ω3-DOCOSAPENTAENOIC
Δ4
22:6n-3
DOCOSAHEXAENOIC
elo
20:3n-3
Δ8

FIG. 1

```
jojobakcs    24 ATLPNFKSSINLHHVKL.GYHYLISNALFLVFIPLLGLASAHLSSFSAHD 72
                .|||    .|  ::| : |  :|:| .    |  | ||   |    ..
ELO2         66 STLPPVLYAITAYYVIIFGGRFLLSKS..KPF.KLNGLFQLHNLVLTSLS 112


jojobakcs    73 LSLLFDLLRRNLLPVVVCSFLFVLLATLHFLTRP 106
                |.||  |:   |.|::|   |:  :  :   |.|
ELO2        113 LTLLL.LMVEQLVPIIVQHGLYFAICNIGAWTQP 145
```

FIG.2

S	T	L	P	P	V	L	Y	A	I	T	A	Y	Y	V	I	I	F	G	G	R	F	L
TCC	ACC	CTC	CCC	CCC	GTC	CTC	TAC	GCC	ATC	ACC	GCC	TAC	TAC	GTC	ATC	ATC	TTC	GGT	GGT	CGC	TTC	CTC
66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88

<-- RO339

L	S	K	S	K	P	F	K	L	N	G	L	F	Q	L	H	N	L	V	L	T	S	L
CTC	TCC	AAG	TCC	AAG	CCC	TTC	AAG	CTC	AAC	GGT	CTC	TTC	CAG	CTC	CAC	AAC	CTC	GTC	CTC	ACC	TCC	CTC
89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111

S	L	T	L	L	L	L	M	V	E	Q	L	V	P	I	I	V	Q	H	G	L	Y	F
TCC	CTC	ACC	CTC	CTC	CTC	CTC	ATG	GTC	GAG	CAG	CTC	GTC	CCC	ATC	ATC	GTC	CAG	CAC	GGT	CTC	TAC	TTC
112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134

A	I	C	N	I	G	A	W	T	Q	P
GCC	ATC	TGC	AAC	ATC	GGT	GCC	TGG	ACC	CAG	CCC
135	136	137	138	139	140	141	142	143	144	145

FIG.3

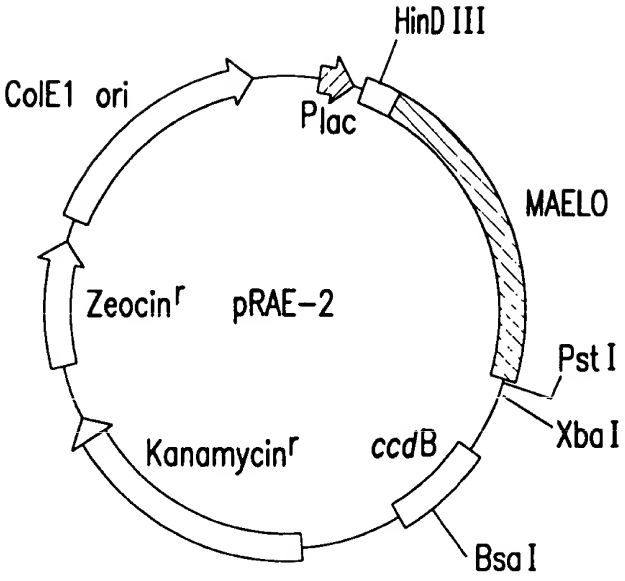
HinD III
ColE1 ori
Plac
MAELO
Zeocin^r
pRAE-2
Pst I
Xba I
Kanamycin^r
ccdB
Bsa I

FIG.4A

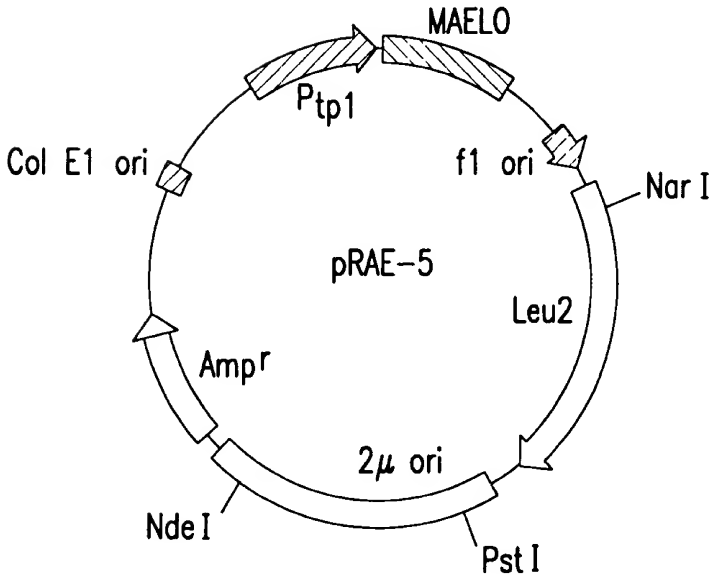
MAELO
Ptp1
Col E1 ori
f1 ori
Nar I
pRAE-5
Leu2
Amp^r
2μ ori
Nde I
Pst I

FIG.4B

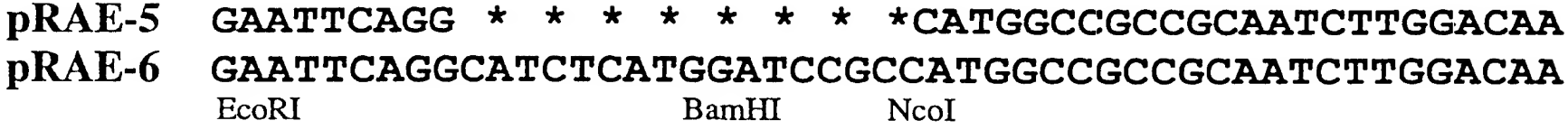
pRAE-5 GAATTCAGG * * * * * * * *CATGGCCGCCGCAATCTTGGACAA
pRAE-6 GAATTCAGGCATCTCATGGATCCGCCATGGCCGCCGCAATCTTGGACAA
EcoRI
BamHI
NcoI

FIG.5

```
  1  ATGGCCGCCG CAATCTTGGA CAAGGTCAAC TTCGGCATTG ATCAGCCCTT
 51  CGGAATCAAG CTCGACACCT ACTTTGCTCA GGCCTATGAA CTCGTCACCG
101  GAAAGTCCAT CGACTCCTTC GTCTTCCAGG AGGGCGTCAC GCCTCTCTCG
151  ACCCAGAGAG AGGTCGCCAT GTGGACTATC ACTTACTTCG TCGTCATCTT
201  TGGTGGTCGC CAGATCATGA AGAGCCAGGA CGCCTTCAAG CTCAAGCCCC
251  TCTTCATCCT CCACAACTTC CTCCTGACGA TCGCGTCCGG ATCGCTGTTG
301  CTCCTGTTCA TCGAGAACCT GGTCCCCATC CTCGCCAGAA ACGGACTTTT
351  CTACGCCATC TGCGACGACG GTGCCTGGAC CCAGCGCCTC GAGCTCCTCT
401  ACTACCTCAA CTACCTGGTC AAGTACTGGG AGTTGGCCGA CACCGTCTTT
451  TTGGTCCTCA AGAAGAAGCC TCTTGAGTTC CTGCACTACT TCCACCACTC
501  GATGACCATG GTTCTCTGCT TTGTCCAGCT TGGAGGATAC ACTTCAGTGT
551  CCTGGGTCCC TATTACCCTC AACTTGACTG TCCACGTCTT CATGTACTAC
601  TACTACATGC GCTCCGCTGC CGGTGTTCGC ATCTGGTGGA AGCAGTACTT
651  GACCACTCTC CAGATCGTCC AGTTCGTTCT TGACCTCGGA TTCATCTACT
701  TCTGCGCCTA CACCTACTTC GCCTTCACCT ACTTCCCCTG GGCTCCCAAC
751  GTCGGCAAGT GCGCCGGTAC CGAGGGTGCT GCTCTCTTTG GCTGCGGACT
801  CCTCTCCAGC TATCTCTTGC TCTTTATCAA CTTCTACCGC ATTACCTACA
851  ATGCCAAGGC CAAGGCAGCC AAGGAGCGTG GAAGCAACTT TACCCCCAAG
901  ACTGTCAAGT CCGGCGGATC GCCCAAGAAG CCCTCCAAGA GCAAGCACAT
951  CTAA
```

FIG.6

```
  1  MAAAILDKVN FGIDQPFGIK LDTYFAQAYE LVTGKSIDSF VFQEGVTPLS
 51  TQREVAMWTI TYFVVIFGGR QIMKSQDAFK LKPLFILHNF LLTIASGSLL
101  LLFIENLVPI LARNGLFYAI CDDGAWTQRL ELLYYLNYLV KYWELADTVF
151  LVLKKKPLEF LHYFHHSMTM VLCFVQLGGY TSVSWVPITL NLTVHVFMYY
201  YYMRSAAGVR IWWKQYLTTL QIVQFVLDLG FIYFCAYTYF AFTYFPWAPN
251  VGKCAGTEGA ALFGCGLLSS YLLLFINFYR ITYNAKAKAA KERGSNFTPK
301  TVKSGGSPKK PSKSKHI*
```

FIG.7

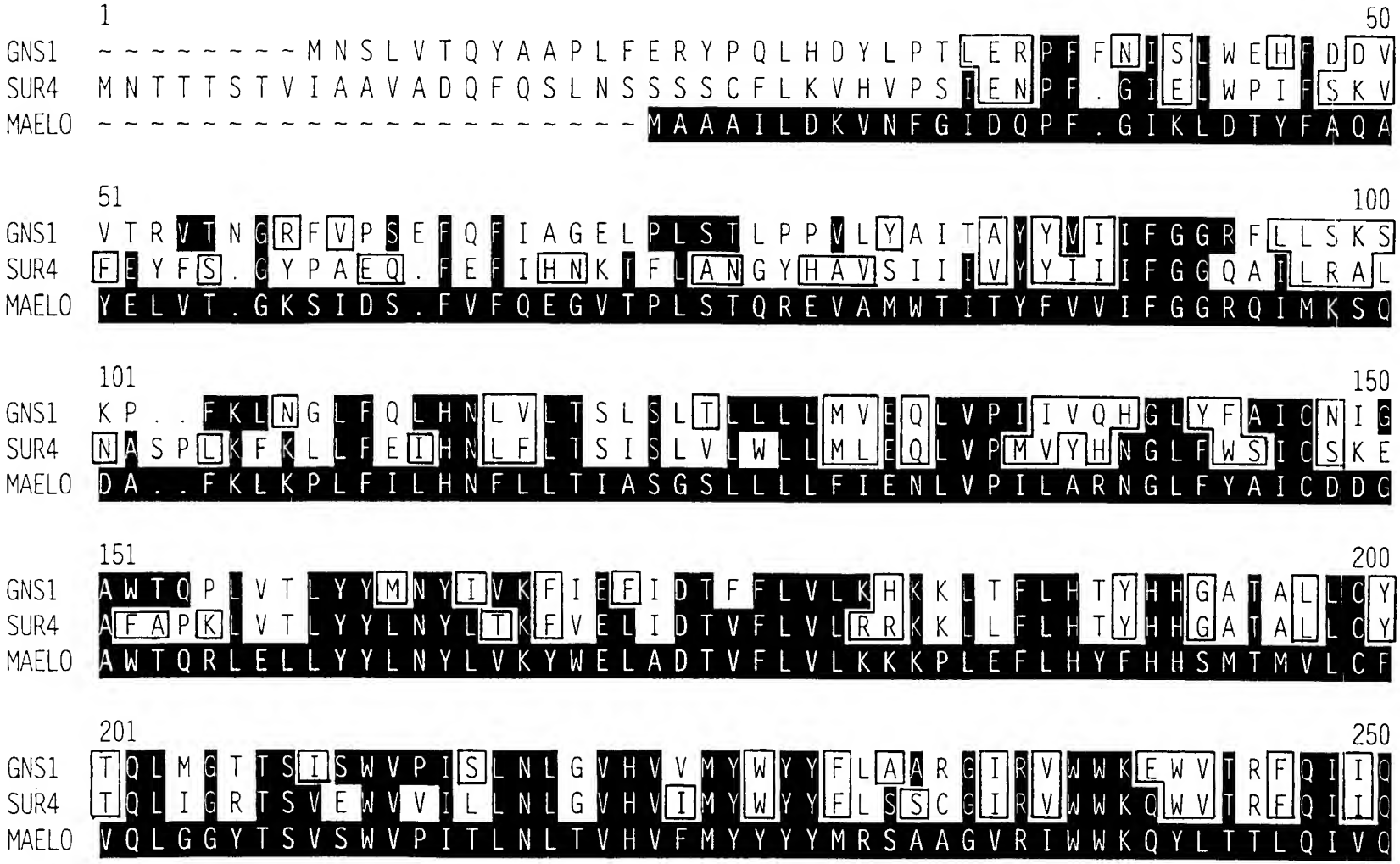
1
50
GNS1 ~~~~~~~~~MNSLVTQYAAPLFERYPQLHDYLPTLERPFFNISLWEHFDDV
SUR4 MNTTTSTVIAAVADQFQSLNSSSSCFLKVHVPSIENPF.GIELWPIFSKV
MAELO ~~~~~~~~~~~~~~~~~~~~~~~~MAAAILDKVNFGIDQPF.GIKLDTYFAQA
51
100
GNS1 VTRVTNGRFVPSEFQFIAGELPLSTLPPVLYAITAYYVIIFGGRFLLSKS
SUR4 FEYFS.GYPAEQ.FEFIHNKTFLANGYHAVSIITVYYIIIFGGQAILRAL
MAELO YELVT.GKSIDS.FVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQ
101
150
GNS1 KP..FKLNGLFQLHNLVLTSLSLTLLLLMVEQLVPIIVQHGLYFAICNIG
SUR4 NASPLKFKLLFEIHNLFLTSISLVLWLLMLEQLVPMVYHNGLFWSICSKE
MAELO DA..FKLKPLFILHNFLLTIASGSLLLLFIENLVPILARNGLFYAICDDG
151
200
GNS1 AWTQPLVTLYYMNYIVKFIEFIDTFFLVLKHKKLTFLHTYHHGATALLCY
SUR4 AFAPKLVTLYYLNYLTKFVELIDTVFLVLRRKKLLFLHTYHHGATALLCY
MAELO AWTQRLELLYYLNYLVKYWELADTVFLVLKKKPLEFLHYFHHSMTMVLCF
201
250
GNS1 TQLMGTTSISWVPISLNLGVHVVMYWYYFLAARGIRVWWKEWVTRFQIIQ
SUR4 TQLIGRTSVEWVVILLNLGVHVIMYWYYFLSSCGIRVWWKQWVTRFQIIQ
MAELO VQLGGYTSVSWVPITLNLTVHVFMYYYYMRSAAGVRIWWKQYLTTLQIVQ

FIG.8A

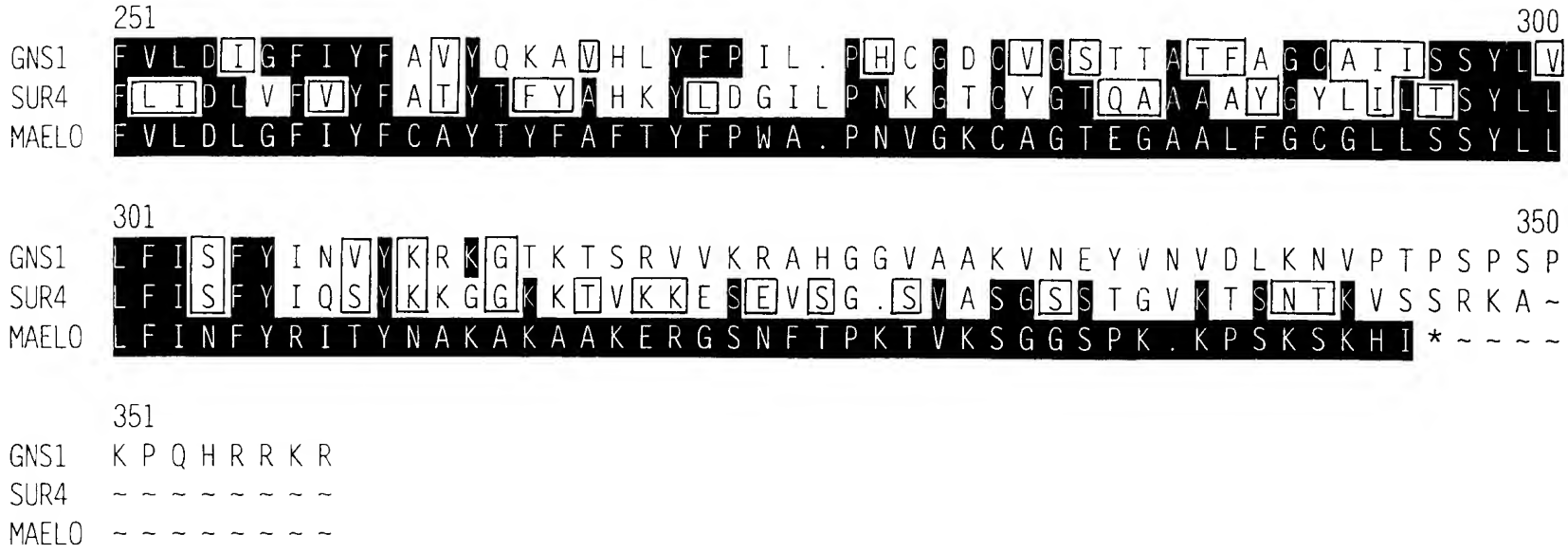
251
300
GNS1 FVLDIGFIYFAVYQKAVHLYFPIL.PHCGDCVGSTTATFAGCAIISSYLV
SUR4 FLIDLVFVYFATYTFYAHKYLDGILPNKGTCYGTQAAAAYGYLILTSYLL
MAELO FVLDLGFIYFCAYTYFAFTYFPWA.PNVGKCAGTEGAALFGCGLLSSYLL
301
350
GNS1 LFISFYINVYKRKGTKTSRVVKRAHGGVAAKVNEYVNVDLKNVPTPSPSP
SUR4 LFISFYIQSYKKGGKKTVKKESEVSG.SVASGSSTGVKTSNTKVSSRKA~
MAELO LFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPK.KPSKSKHI*~~~~
351
GNS1 KPQHRRKR
SUR4 ~~~~~~~~
MAELO ~~~~~~~~

FIG.8B

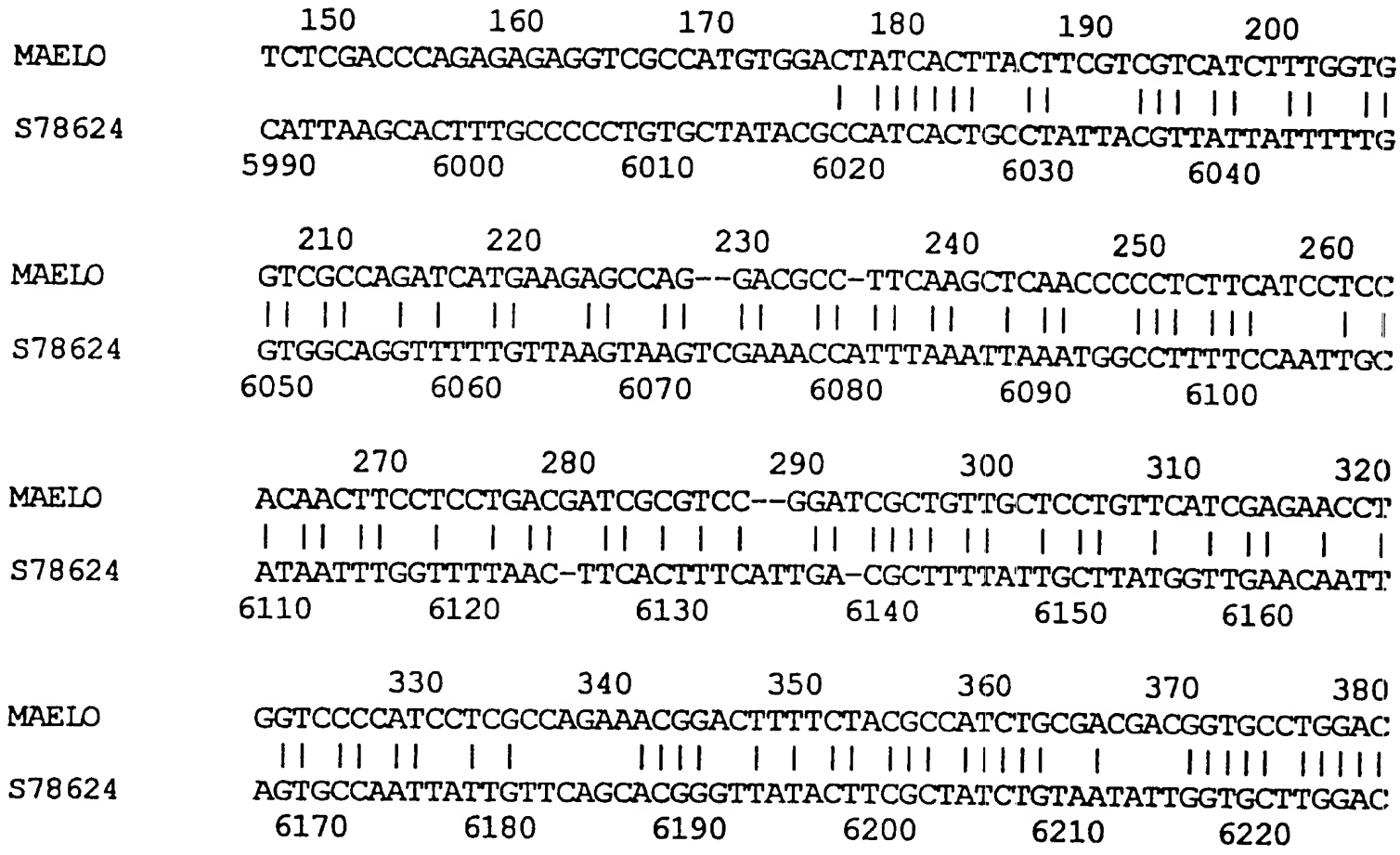
150 160 170 180 190 200
MAELO TCTCGACCCAGAGAGAGGTCGCCATGTGGACTATCACTTACTTCGTCGTCATCTTTGGTG
S78624 CATTAAGCACTTTGCCCCCTGTGCTATACGCCATCACTGCCTATTACGTTATTATTTTTG
5990 6000 6010 6020 6030 6040
210 220 230 240 250 260
MAELO GTCGCCAGATCATGAAGAGCCAG--GACGCC-TTCAAGCTCAACCCCCTCTTCATCCTCC
S78624 GTGGCAGGTTTTTGTTAAGTAAGTCGAAACCATTTAAATTAAATGGCCTTTTCCAATTGC
6050 6060 6070 6080 6090 6100
270 280 290 300 310 320
MAELO ACAACTTCCTCCTGACGATCGCGTCC--GGATCGCTGTTGCTCCTGTTCATCGAGAACCT
S78624 ATAATTTGGTTTTAAC-TTCACTTTCATTGA-CGCTTTTATTGCTTATGGTTGAACAATT
6110 6120 6130 6140 6150 6160
330 340 350 360 370 380
MAELO GGTCCCCATCCTCGCCAGAAACGGACTTTTCTACGCCATCTGCGACGACGGTGCCTGGAC
S78624 AGTGCCAATTATTGTTCAGCACGGGTTATACTTCGCTATCTGTAATATTGGTGCTTGGAC
6170 6180 6190 6200 6210 6220

FIG.9A

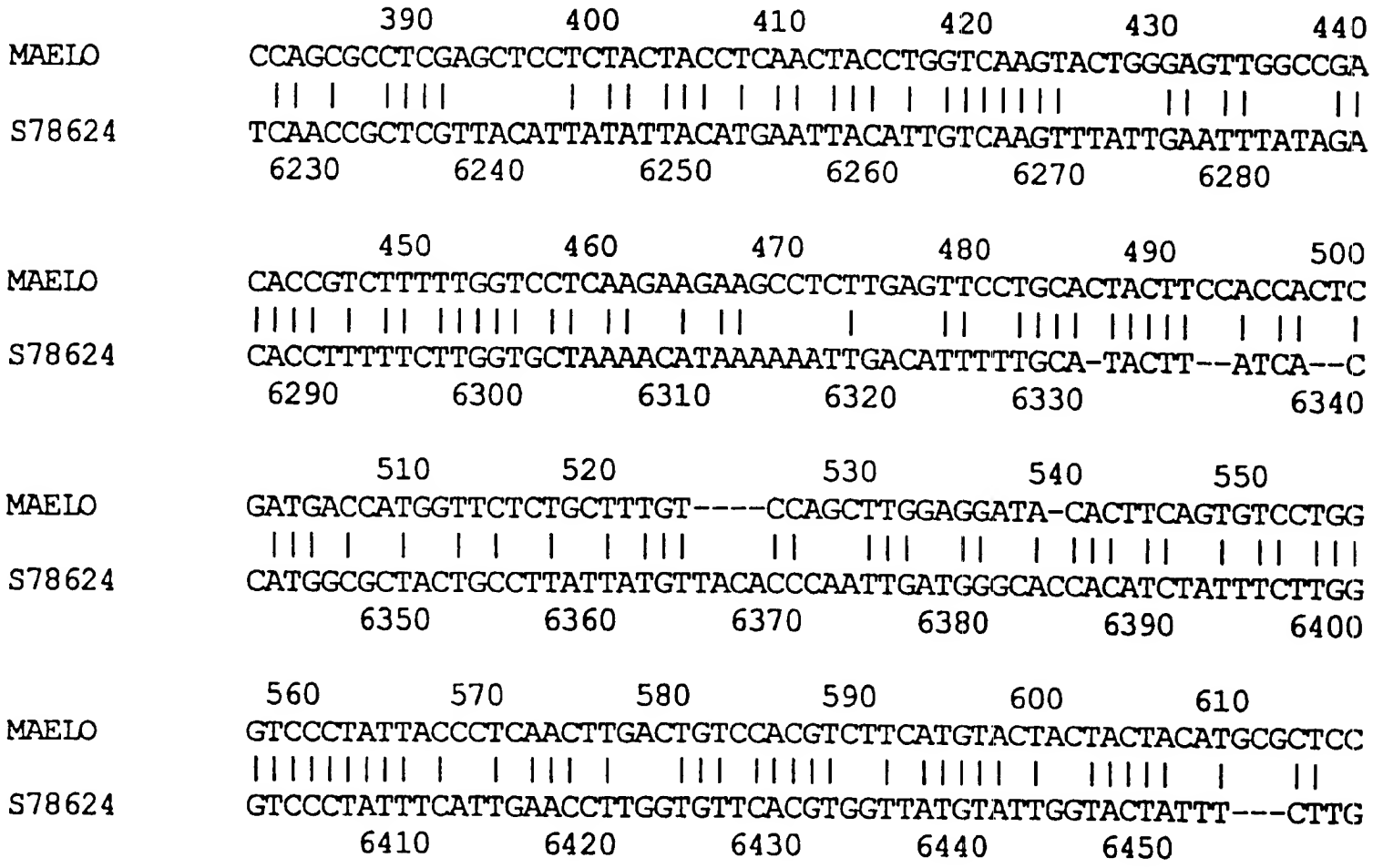
390 400 410 420 430 440
MAELO CCAGCGCCTCGAGCTCCTCTACTACCTCAACTACCTGGTCAAGTACTGGGAGTTGGCCGA
S78624 TCAACCGCTCGTTACATTATATTACATGAATTACATTGTCAAGTTTATTGAATTTATAGA
6230 6240 6250 6260 6270 6280
450 460 470 480 490 500
MAELO CACCGTCTTTTTGGTCCTCAAGAAGAAGCCTCTTGAGTTCCTGCACTACTTCCACCACTC
S78624 CACCTTTTTCTTGGTGCTAAAACATAAAAAATTGACATTTTTGCA-TACTT--ATCA--C
6290 6300 6310 6320 6330 6340
510 520 530 540 550
MAELO GATGACCATGGTTCTCTGCTTTGT----CCAGCTTGGAGGATA-CACTTCAGTGTCCTGG
S78624 CATGGCGCTACTGCCTTATTATGTTACACCCAATTGATGGGCACCACATCTATTTCTTGG
6350 6360 6370 6380 6390 6400
560 570 580 590 600 610
MAELO GTCCCTATTACCCTCAACTTGACTGTCCACGTCTTCATGTACTACTACTACATGCGCTCC
S78624 GTCCCTATTTCATTGAACCTTGGTGTTCACGTGGTTATGTATTGGTACTATTT---CTTG
6410 6420 6430 6440 6450

FIG.9B


620 630 640 650 660 670
MAELO GCTGCC——GGTGTTCGCATCTGGTGGAAGCAGTACTTGACCACTCTCCAGATCGTCCAG
S78624 GCTGCCAGAGGCATCAGGGTCTGGTGGAAGGAATGGGTTACCAGATTTCAAATTATCCAA
6460 6470 6480 6490 6500 6510
680 690 700 710 720 730
MAELO TTCGTTCTTGACCTCGGATTCATCTACTTCTGCGCCTACACCTACTTCGCCTTCACCTAC
S78624 TTTGTTTTGGATATCGGTTTCATATATTTTGCTGTCTACCAAAAAGCAGTTCACTTGTAT
6520 6530 6540 6550 6560 6570

FIG.9C

Host(plasmid)	334(pCGN7875)	334(pYES2)	334(pYX242)	334(pRAE-5)	334(pRAE-6)	334(pYX242)	334(pRAE-5)
Added substrate	25 µM OA	25 µM OA	25 µM GLA	25 µM GLA	25 µM GLA	no substrate	no substrate
Fatty acid	lipid (µg)	lipid (µg)	lipid (µg)	lipid (µg)	lipid (µg)	lipid (µg)	lipid (µg)
C16:0	11.948	23.601	35.123	92.011	85.160	16.294	25.34
C16:1	30.665	71.217	32.789	315.464	115.456	56.183	113.913
C18:0	6.185	9.704	10.515	22.628	18.879	5.535	11.092
C18:1n-9	35.340	57.429	33.989	154.386	106.881	28.388	51.538
C18:3n-6			48.856	58.084	12.434		
C20:0			0.474	0.710	0.244		
C20:1n-9	**(0.375%)* 0.352**	**(0.309%)* 0.527**		1.405	0.867		0.516
C20:3n-6	**ND**	**ND**	**(0.092%)* 0.226**	**(0.324%)* 2.504**	**(0.269%)* 1.006**	**ND**	**ND**
C22:0				0.460			
C22:1n-9				0.321	0.315		
C24:0					1.825		0.999
Total Lipid	93.760	170.490	245.090	771.690	374.420	112.99	256.52
ND = Not Detected							
*% total fatty acid							

FIG.10A

Host(plasmid)	334(pYX242)	334(pYX242)	334(pRAE-5)	334(pRAE-5)	334(pRAE-6)
Added substrate	25 µM GLA	25 µM GLA	25 µM GLA	25 µM GLA	25 µM GLA
Fatty acid	lipid (µg)	lipid (µg)	lipid (µg)	lipid (µg)	lipid (µg)
C16:0	60.683	61.487	100.998	96.193	66.761
C16:1	79.838	79.586	359.754	220.440	87.359
C18:0	9.784	10.106	15.317	15.165	16.744
C18:1n-9	38.536	39.936	108.472	89.637	71.631
C18:3n-6	17.974	17.833	82.866	56.596	17.766
C20:0			0.510	0.570	
C20:1n-9					
C20:3n-6	**(0.136%)* 0.389**	**(0.130%)* 0.374**	**(0.336%)* 3.035**	**(0.401%)* 2.689**	**(0.353%)* 1.185**
C22:0			0.414		
C22:1n-9				0.383	
C24:0			1.513	1.626	
Total Lipid	285.560	288.045	902.560	671.113	335.496
*% total fatty acid					

FIG.10B

Host(plasmid)	334(pRAE-5/pCGR4)	334(pYX242/pYES2)		Host(plasmid)	334(pRAE-5/pCGR4)	334(pYX242/pYES2)
Added substrate	25 µM GLA	25 µM GLA		Added substrate	25 µM GLA	25 µM GLA
Fatty Acid	lipid (µg)	lipid (µg)			lipid (µg)	lipid (µg)
C16:0	41.050	37.169		C16:0	96.986	32.221
C16:1	99.393	100.552		C16:1n-7	209.667	62.757
C18:0	34.432	27.852		C18:0	80.418	14.027
C18:1	110.631	92.786		C18:1n-9	207.104	28.701
C18:3n-6	**15.004**	**7.924**		**C18:3n-6**	**25.264**	**10.543**
C20:0	0.643	0.574		C20:0	2.038	
C20:1	1.996	1.684		C20:1n-9	3.591	
C20:3n-6	**0.542**	**0.607**		**C20:3n-6**	**1.284**	**0.326**
C20:4n-6	**0.579**			**C20:4n-6**	**1.392**	
C22:0	1.242	2.604		C22:0	1.124	
C24:0	4.754	4.563		C24:0	3.952	
Total Lipid	334	300		Total Lipid	756	197

FIG.11

Host(plasmid)	334(pYX242)	334(pRAE-5)	334(pRELO-1)	334(pRELO-2)
Added substrate	25 μM GLA	25 μM GLA	25 μM GLA	25 μM GLA
	25°C/48hrs	25°C/48hrs	25°C/48hrs	25°C/48hrs
Fatty acid	lipid (μg)	lipid (μg)	lipid (μg)	lipid (μg)
C16:0	28.7	76.707	84.424	77.445
C16:1	0.729	2.513	1.532	1.056
C18:0	7.432	15.761	27.17	21.32
C18:1n-9	28.9	77.323	109.419	82.844
C18:3n-6	9.729	29.236	19.085	**18.804**
C20:0		0.643	0.522	0.537
C20:1n-9		0.77	0.426	0.299
C20:3n-6	**(0.185%)* 0.374**	**(0.279%)* 1.472**	**(0.153%)* 0.748**	**(0.200%)* 0.832**
C22:0		0.451		
C22:1n-9			0.224	
C24:0		0.918		
Total Lipid	202	527	490	416
*%total fatty acid				

FIG.12

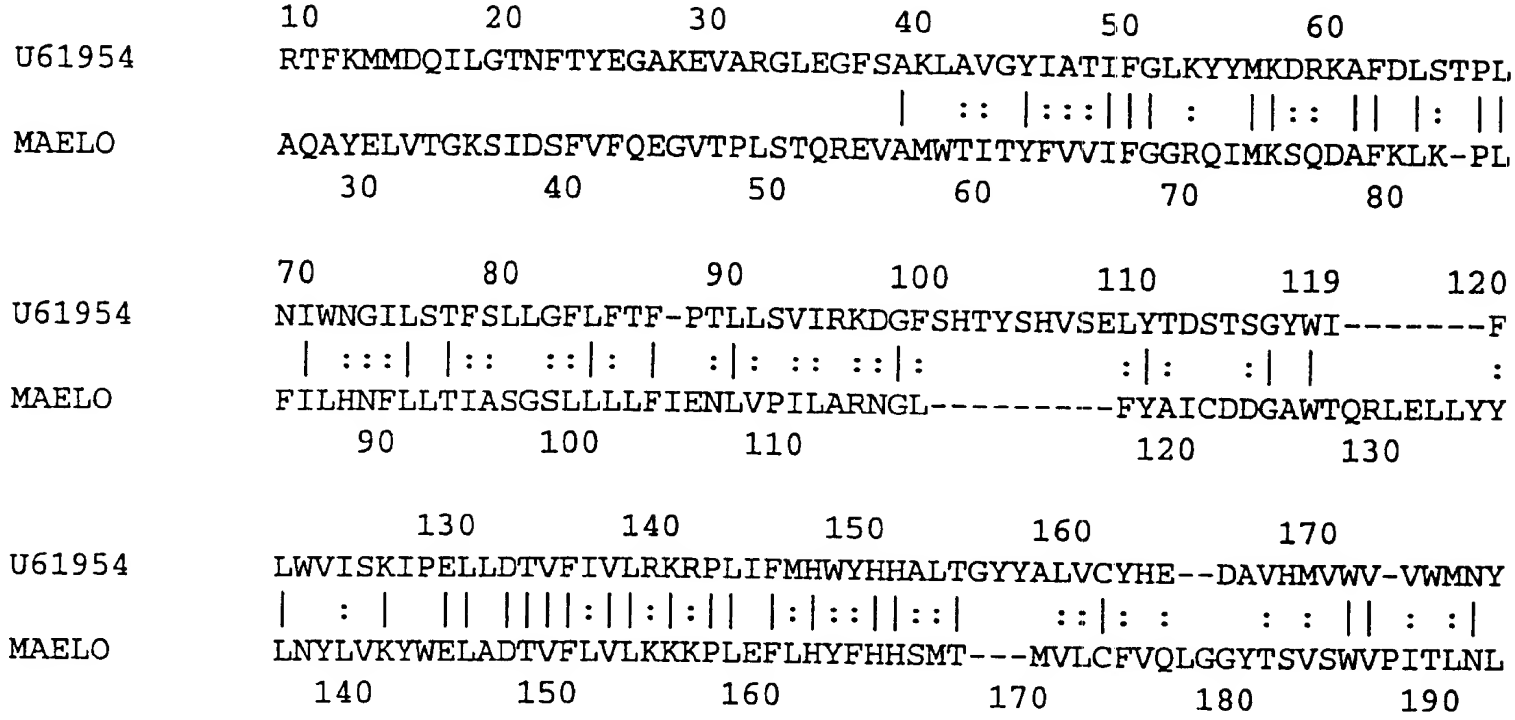
10 20 30 40 50 60
U61954 RTFKMMDQILGTNFTYEGAKEVARGLEGFSAKLAVGYIATIFGLKYYMKDRKAFDLSTPL
MAELO AQAYELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLK-PL
30 40 50 60 70 80
70 80 90 100 110 119 120
U61954 NIWNGILSTFSLLGFLFTF-PTLLSVIRKDGFSHTYSHVSELYTDSTSGYWI-------F
MAELO FILHNFLLTIASGSLLLLFIENLVPILARNGL---------FYAICDDGAWTQRLELLYY
90 100 110 120 130
130 140 150 160 170
U61954 LWVISKIPELLDTVFIVLRKRPLIFMHWYHHALTGYYALVCYHE--DAVHMVWV-VWMNY
MAELO LNYLVKYWELADTVFLVLKKKPLEFLHYFHHSMT---MVLCFVQLGGYTSVSWVPITLNL
140 150 160 170 180 190

FIG. 13A

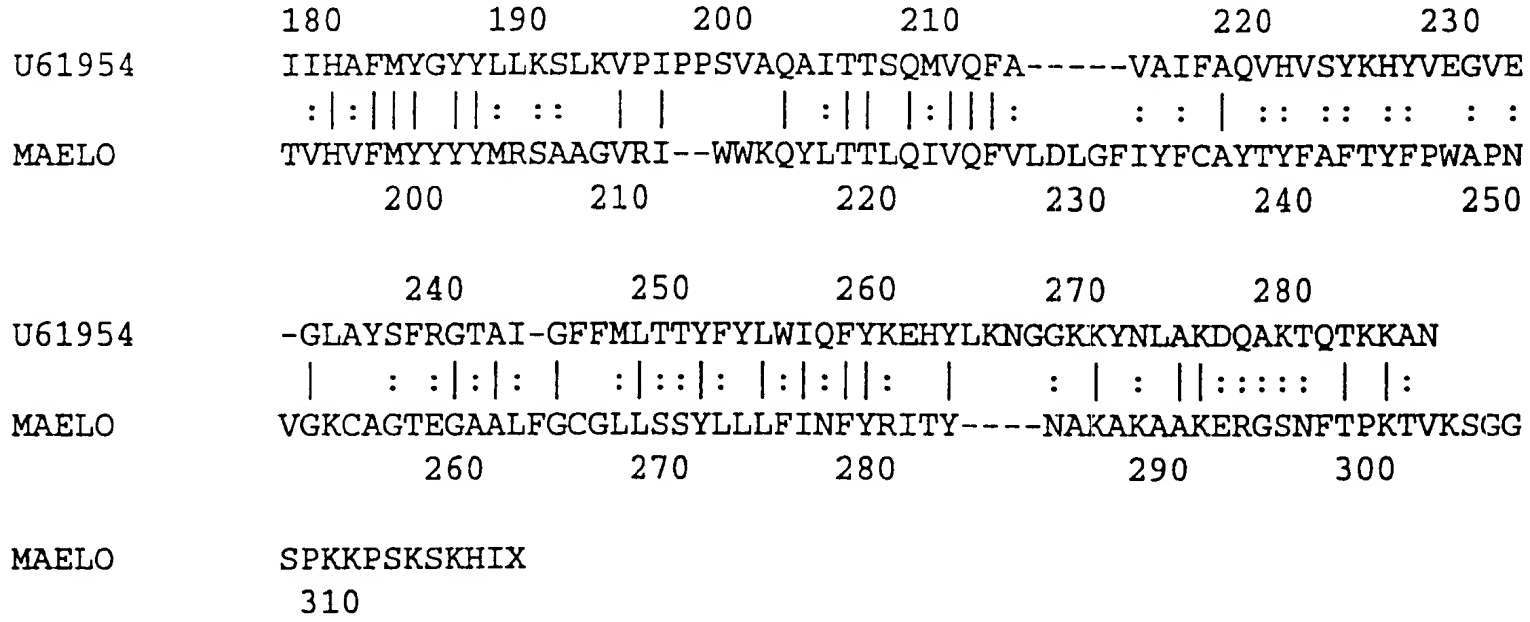
180 190 200 210 220 230
U61954 IIHAFMYGYYLLKSLKVPIPPSVAQAITTSQMVQFA-----VAIFAQVHVSYKHYVEGVE
MAELO TVHVFMYYYYMRSAAGVRI--WWKQYLTTLQIVQFVLDLGFIYFCAYTYFAFTYFPWAPN
200 210 220 230 240 250
240 250 260 270 280
U61954 -GLAYSFRGTAI-GFFMLTTYFYLWIQFYKEHYLKNGGKKYNLAKDQAKTQTKKAN
MAELO VGKCAGTEGAALFGCGLLSSYLLLFINFYRITY----NAKAKAAKERGSNFTPKTVKSGG
260 270 280 290 300
MAELO SPKKPSKSKHIX
310

FIG. 13B

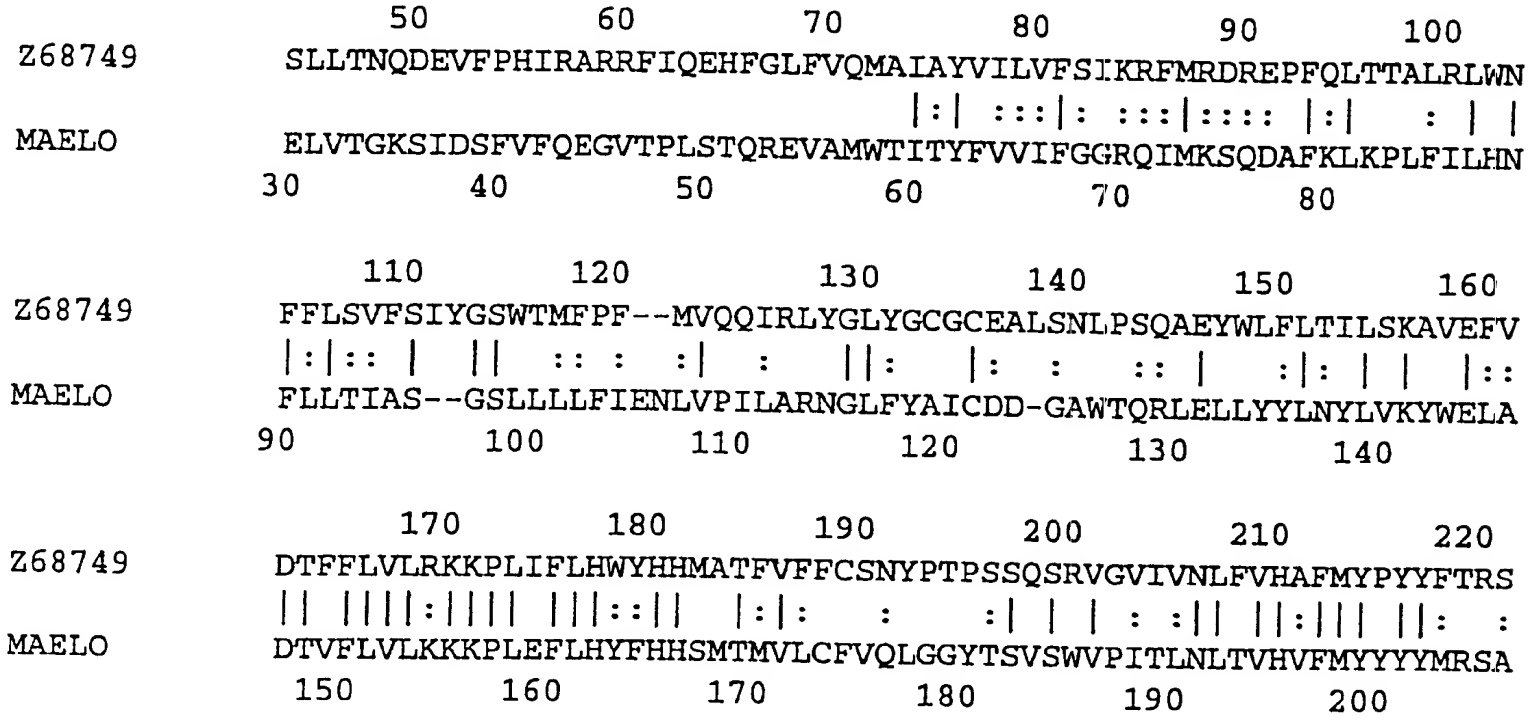
50 60 70 80 90 100
Z68749 SLLTNQDEVFPHIRARRFIQEHFGLFVQMAIAYVILVFSIKRFMRDREPFQLTTALRLWN
MAELO ELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFILHN
30 40 50 60 70 80
110 120 130 140 150 160
Z68749 FFLSVFSIYGSWTMFPF--MVQQIRLYGLYGCGCEALSNLPSQAEYWLFLTILSKAVEFV
MAELO FLLTIAS--GSLLLLFIENLVPILARNGLFYAICDD-GAWTQRLELLYYLNYLVKYWELA
90 100 110 120 130 140
170 180 190 200 210 220
Z68749 DTFFLVLRKKPLIFLHWYHHMATFVFFCSNYPTPSSQSRVGVIVNLFVHAFMYPYYFTRS
MAELO DTVFLVLKKKPLEFLHYFHHSMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYYMRSA
150 160 170 180 190 200

FIG. 14A

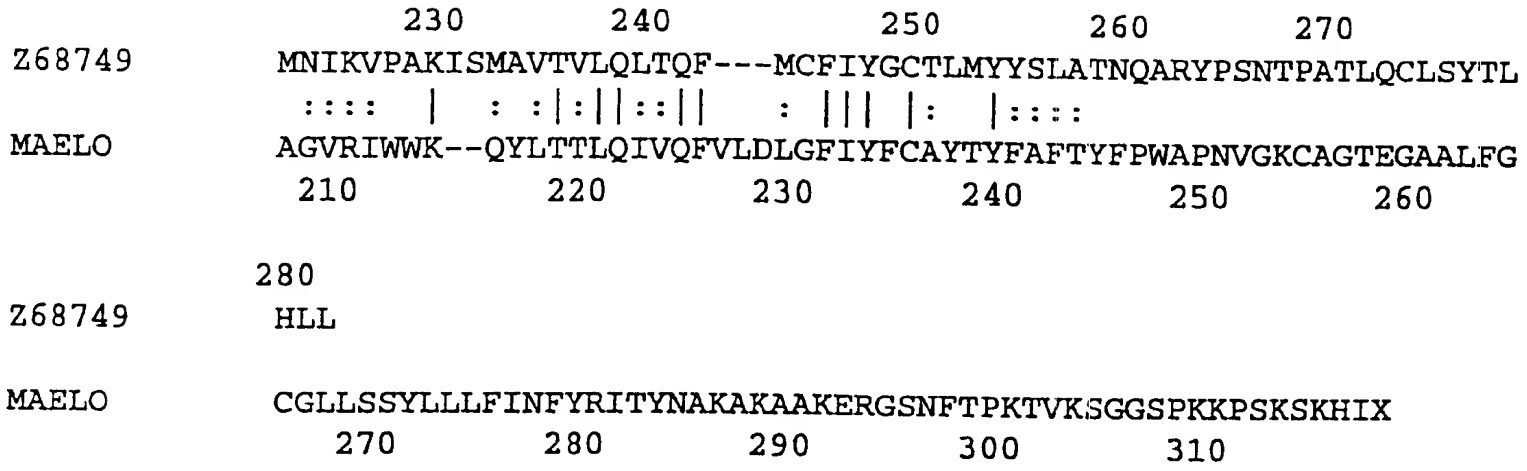
230 240 250 260 270
Z68749 MNIKVPAKISMAVTVLQLTQF---MCFIYGCTLMYYSLATNQARYPSNTPATLQCLSYTL
MAELO AGVRIWWK--QYLTTLQIVQFVLDLGFIYFCAYTYFAFTYFPWAPNVGKCAGTEGAALFG
210 220 230 240 250 260
280
Z68749 HLL
MAELO CGLLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHIX
270 280 290 300 310

FIG. 14B

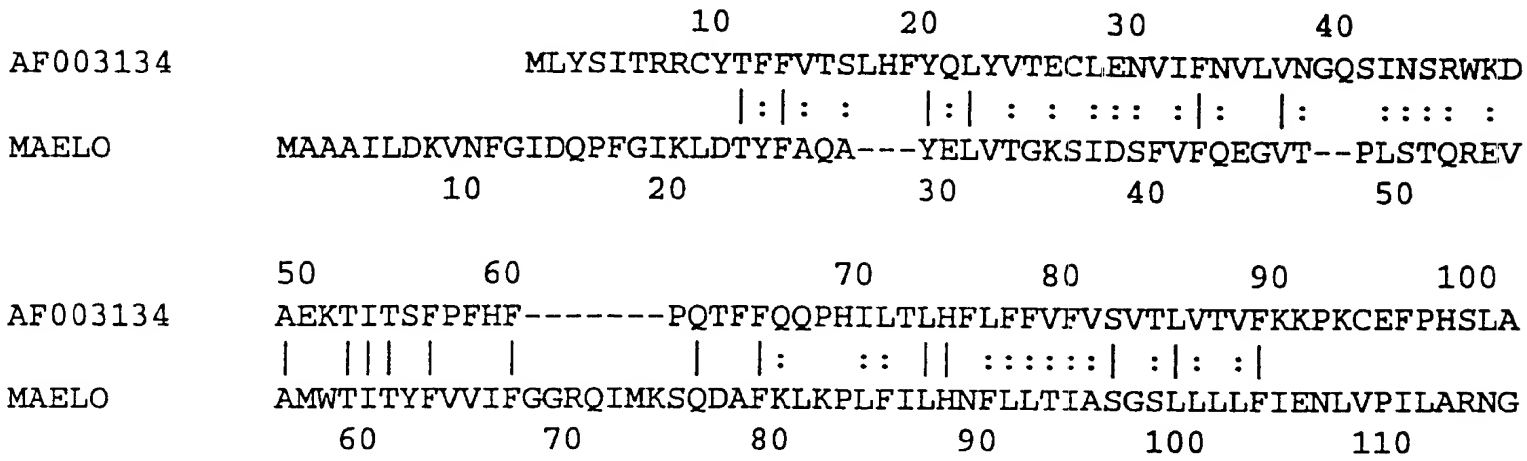
10 20 30 40
AF003134 MLYSITRRCYTFFVTSLHFYQLYVTECLENVIFNVLVNGQSINSRWKD
MAELO MAAAILDKVNFGIDQPFGIKLDTYFAQA---YELVTGKSIDSFVFQEGVT--PLSTQREV
10 20 30 40 50
50 60 70 80 90 100
AF003134 AEKTITSFPFHF-------PQTFFQQPHILTLHFLFFVFVSVTLVTVFKKPKCEFPHSLA
MAELO AMWTITYFVVIFGGRQIMKSQDAFKLKPLFILHNFLLTIASGSLLLLFIENLVPILARNG
60 70 80 90 100 110

FIG.15

Mouse

```
                          10          20          30       39       40
U97107          MDTSMNFSRGLKMD--LMQPYDFETFQDLRPFLEEYWVSSF-------LIVV
                         |:|:|  : | |:: | :::  |: :  |: :       : ::
MAELO       MAAAILDKVNFGIDQPFGIKLDTYFAQAYELVTGKSIDSFVFQEGVTPLSTQREVAMWTI
                   10        20        30        40        50        60

                50        60        70        80        90       100
U97107      VYLLLIVVGQTYMRTRKSFSLQRPLILWSFFLAIFSILGTLRMWKFMATVMFTVGLKQTV
            :|:::|  |:  |::: :|:|:  :|| :|:|:|  |  |:| :  |: ::: : :: :
MAELO       TYFVVIFGGRQIMKSQDAFKLKPLFILHNFLLTIAS--GSL-LLLFIENLV-PILARNGL
                   70        80        90          100       110

               110       120         130       140       150
U97107      CFAIYTDDAVVRFWSFLFLLSKVV---ELGDTAFIILRKRPLIFVHWYHHST--VLLFTS
             :||  | | ::   :|: |: :|   ||:||:|::|:|:|| |:|::|||   || |::
MAELO       FYAICDDGAWTQRLELLYYLNYLVKYWELADTVFLVLKKKPLEFLHYFHHSMTMVLCFVQ
             120       130       140       150       160       170
```

FIG. 16A

Mouse

```
                160       170       180       190       200       210
U97107          FGYKNKVPSGGWF-MTMNFGVHSVMYTYYTMKAAKLKHPNLLPMVITSLQILQMVLG---
                :|  ::|   :|  :|:|: ||  || ||  :|| ::      : :|:|||:|:||
MAELO           LGGYTSV---SWVPITLNLTVHVFMYYYYMRSAAGVR--IWWKQYLTTLQIVQFVLDLGF
                 180          190       200       210          220       230

                        220       230       240       250       260
U97107          ------TIFGILNYIWRQEKG-CHTTTEHFFWSFMLYGTYFILFAHFFHRAYLRPKGKVA
                      | |::  : |  : | |  |    :::  | ::|::|| :|:: :|   |:|:|
MAELO           IYFCAYTYFAFTYFPWAPNVGKCAGTEGAALFGCGLLSSYLLLFINFYRITY-NAKAKAA
                      240       250       260       270       280       290

                270
U97107          SKSQX
                ::
MAELO           KERGSNFTPKTVKSGGSPKKPSKSKHIX
                       300       310
```

FIG. 16B

Human

```
                 110        120        130        140        150        160
MAELO            NLVPILARNGLFYAICDDGAWTQRLELLYYLNYLVKYWELADTVFLVLKKKPLEFLHYFH
                                                |:||:     :||:|::|:|: | |||::|
AC004050                                  SLLVVKDLTYLLPLCLPGDTIFIILRKQKLIFLHWYH
                                                  10         20         30

                 170        180        190        200        210        220
MAELO            HSMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYYMRSAAGVRIWWK--QYLTTLQIV
                 |  :::  : :   ::: :   :|:|  ||: || ||   ||| |:  |  :::|  ||:
AC004050         HITVLLYSWYSYKDMVAGGGWFMTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSQIT
                  40         50         60         70         80         90

                     230        240        250        260        270        280
MAELO            QFVLDLGFIYFCAYTYFAFTYFPWAPNVGKCAGTEGAALFGCGLLSSYLLLFINFYRITY
                 |:::       |: :|::|    |  :  :| :     :::  :  |||:|| :|:  :|
AC004050         QMLMG------CVVNYLVFC---WMQH-DQCHSHFQNIFWSSLMYLSYLVLFCHFFFEAY
                 100             110           120        130        140
```

FIG. 16C

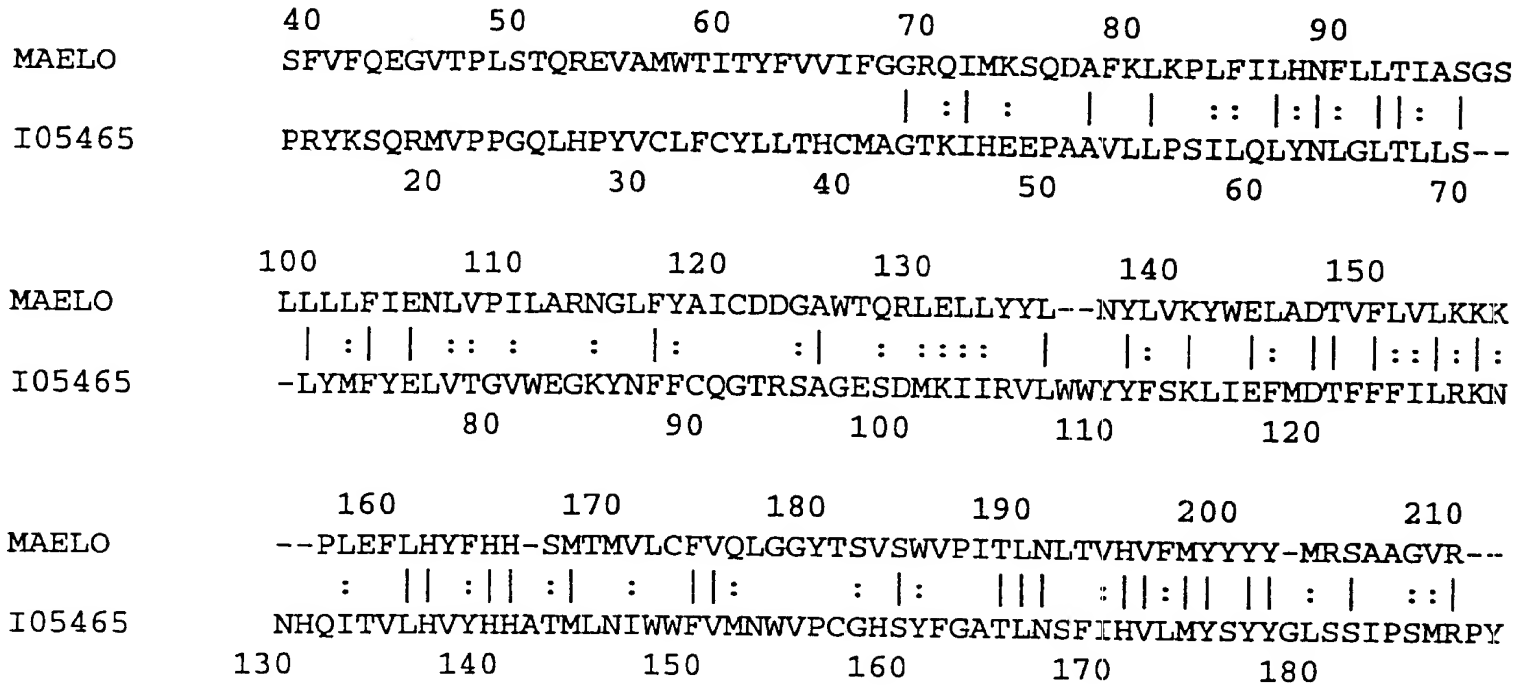
40 50 60 70 80 90
MAELO SFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFILHNFLLTIASGS
I05465 PRYKSQRMVPPGQLHPYVCLFCYLLTHCMAGTKIHEEPAAVLLPSILQLYNLGLTLLS--
20 30 40 50 60 70
100 110 120 130 140 150
MAELO LLLLFIENLVPILARNGLFYAICDDGAWTQRLELLYYL--NYLVKYWELADTVFLVLKKK
I05465 -LYMFYELVTGVWEGKYNFFCQGTRSAGESDMKIIRVLWWYYFSKLIEFMDTFFFILRKN
80 90 100 110 120
160 170 180 190 200 210
MAELO --PLEFLHYFHH-SMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYY-MRSAAGVR--
I05465 NHQITVLHVYHHATMLNIWWFVMNWVPCGHSYFGATLNSFIHVLMYSYYGLSSIPSMRPY
130 140 150 160 170 180

FIG. 17A

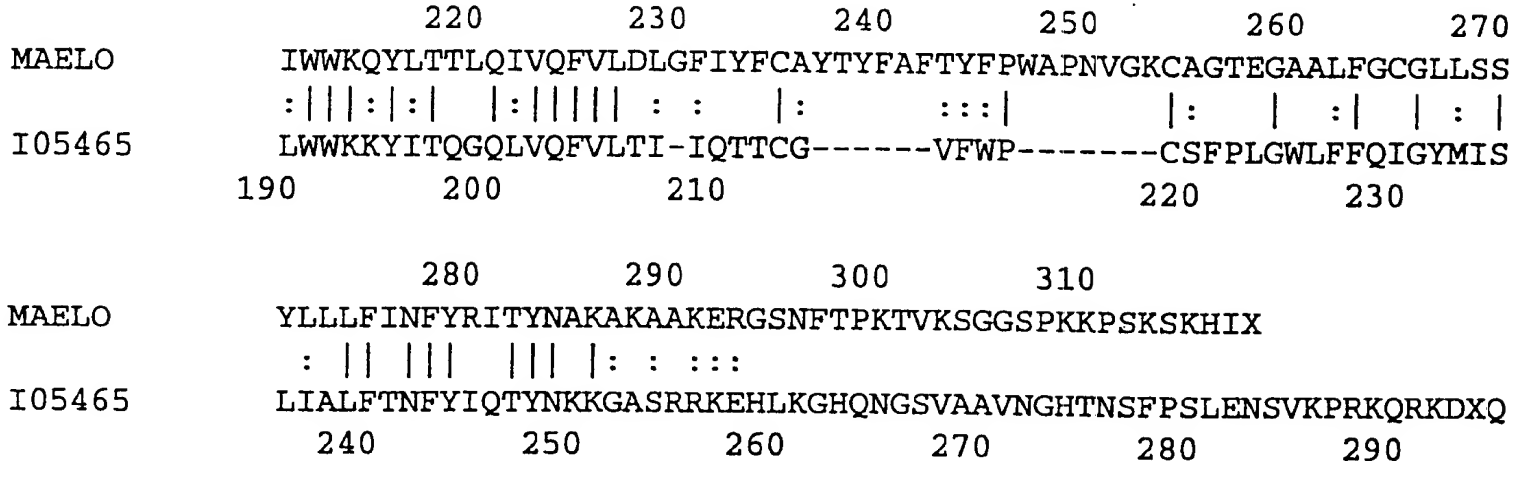
220 230 240 250 260 270
MAELO IWWKQYLTTLQIVQFVLDLGFIYFCAYTYFAFTYFPWAPNVGKCAGTEGAALFGCGLLSS
I05465 LWWKKYITQGQLVQFVLTI-IQTTCG------VFWP-------CSFPLGWLFFQIGYMIS
190 200 210 220 230
280 290 300 310
MAELO YLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHIX
I05465 LIALFTNFYIQTYNKKGASRRKEHLKGHQNGSVAAVNGHTNSFPSLENSVKPRKQRKDXQ
240 250 260 270 280 290

FIG. 17B

```
  1  MGTDQGKTFT WEELAAHNTK DDLLLAIRGR VYDVTKFLSR HPGGVDTLLL
 51  GAGRDVTPVF EMYHAFGAAD AIMKKYYVGT LVSNELPIFP EPTVFHKTIK
101  TRVEGYFTDR NIDPKNRPEI WGRYALIFGS LIASYYAQLF VPFVVERTWL
151  QVVFAIIMGF ACAQVGLNPL HDASHFSVTH NPTVWKILGA THDFFNGASY
201  LVWMYQHMLG HHPYTNIAGA DPDVSTSEPD VRRIKPNQKW FVNHINQHMF
251  VPFLYGLLAF KVRIQDINIL YFVKTNDAIR VNPISTWHTV MFWGGKAFFV
301  WYRLIVPLQY LPLGKVLLLF TVADMVSSYW LALTFQANHV VEEVQWPLPD
351  ENGIIQKDWA AMQVETTQDY AHDSHLWTSI TGSLNYQAVH HLFPNVSQHH
401  YPDILAIIKN TCSEYKVPYL VKDTFWQAFA SHLEHLRVLG LRPKEE*
```

FIG.18

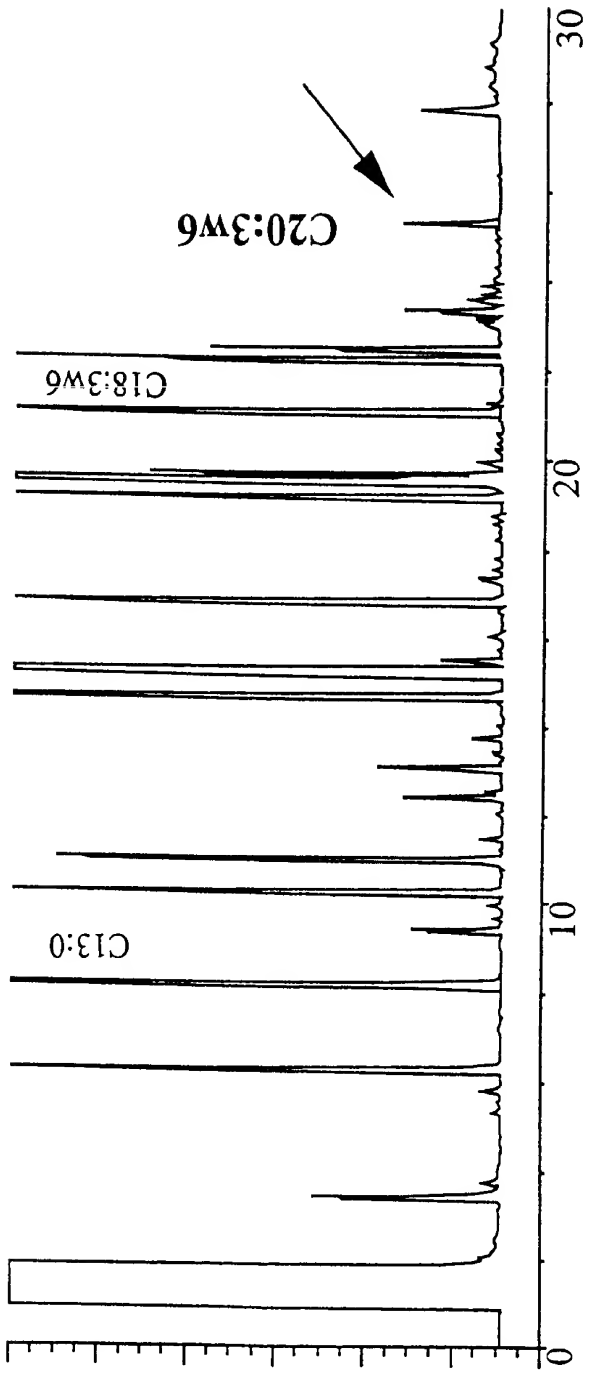

FIG.19

Host(plasmid)	334(MAD708-2)	334 (MAD708-10)	334(MAD708-18)	334 (MAD708-19)	334(MAD708-30)	334 (pRAE5)
Added substrate	25μM GLA	25μM GLA	25μM GLA	25μM GLA	25μM GLA	25μM GLA
Fatty Acid	% total lipid					
C16:0	14.1	14.68	14.38	15.45	14.13	13.59
C16:1	42.84	43.42	42.57	38.03	43.58	43.98
C18:0	3.19	3.28	3.63	4.08	3.37	2.04
C18:1n-9	17.66	19.39	19.6	20.8	20.06	10.88
C18:3n-6	**6.65**	**5.58**	**10.24**	**9.46**	**3.56**	**11.14**
C20:0	0.26	0.3	0.32	0.4	0.46	0.57
C20:3n-6	**(47.5%) 6.03**	**(41.2%) 3.92**	**(8.0%) 0.91**	**(21.5%) 2.59**	**(49%) 3.43**	**(3.4%) 0.24**
Total Lipid (μg)	238.47	307.86	188.51	167.31	207.47	466.65

(% conversion) = product/(substrate+product)

FIG.20

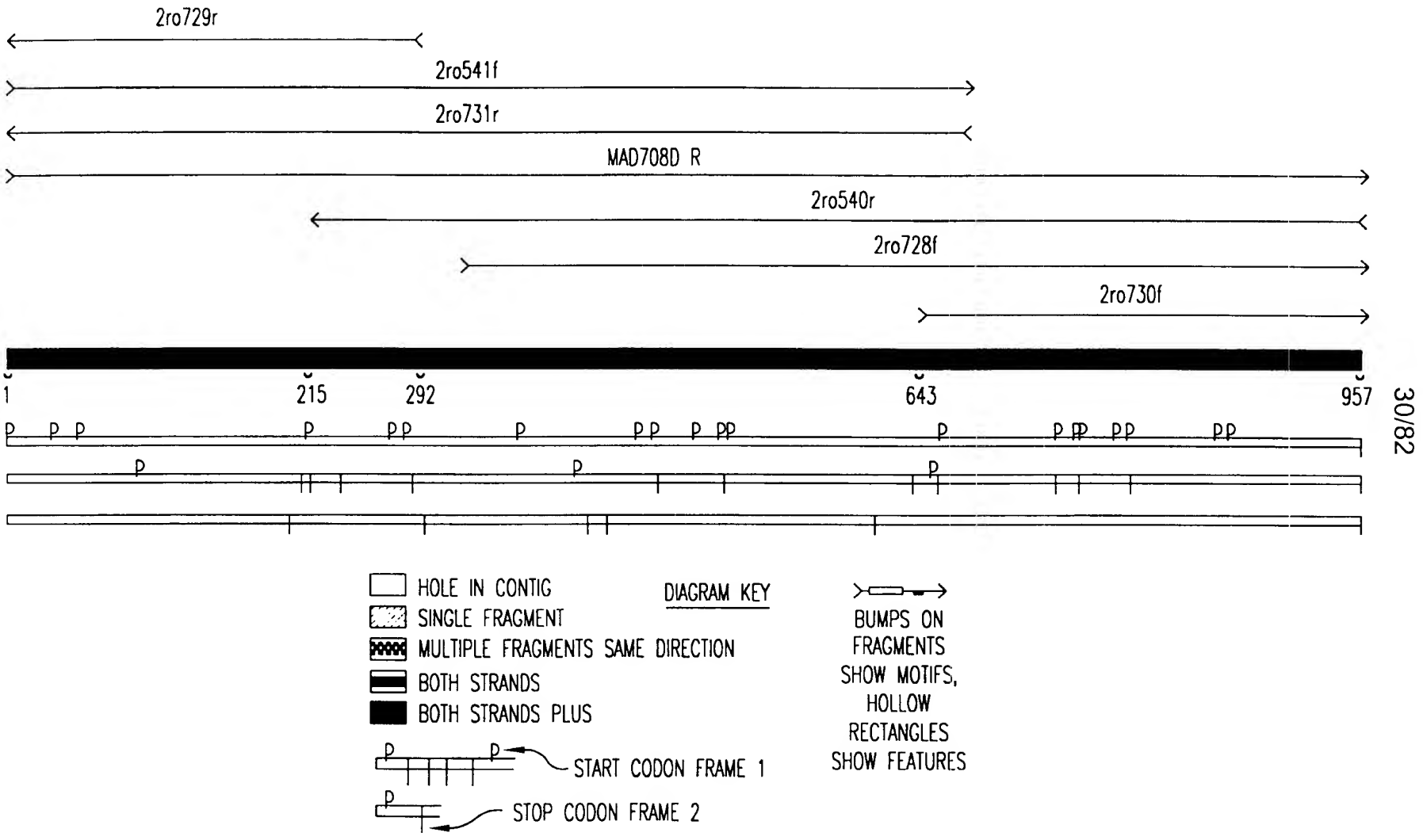
2ro729r
2ro541f
2ro731r
MAD708D R
2ro540r
2ro728f
2ro730f
1
215
292
643
957
DIAGRAM KEY
HOLE IN CONTIG
SINGLE FRAGMENT
MULTIPLE FRAGMENTS SAME DIRECTION
BOTH STRANDS
BOTH STRANDS PLUS
START CODON FRAME 1
STOP CODON FRAME 2
BUMPS ON FRAGMENTS SHOW MOTIFS, HOLLOW RECTANGLES SHOW FEATURES

FIG.21

```
  1  ATGGAGTCGA TTGCGCCATT CCTCCCATCA AAGATGCCGC AAGATCTGTT
 51  TATGGACCTT GCCACCGCTA TCGGTGTCCG GGCCGCGCCC TATGTCGATC
101  CTCTCGAGGC CGCGCTGGTG GCCCAGGCCG AGAAGTACAT CCCCACGATT
151  GTCCATCACA CGCGTGGGTT CCTGGTCGCG GTGGAGTCGC CTTTGGCCCG
201  TGAGCTGCCG TTGATGAACC CGTTCCACGT GCTGTTGATC GTGCTCGCTT
251  ATTTGGTCAC GGTCTTTGTG GGCATGCAGA TCATGAAGAA CTTTGAGCGG
301  TTCGAGGTCA AGACGTTTTC GCTCCTGCAC AACTTTTGTC TGGTCTCGAT
351  CAGCGCCTAC ATGTGCGGTG GGATCCTGTA CGAGGCTTAT CAGGCCAACT
401  ATGGACTGTT TGAGAACGCT GCTGATCATA CCTTCAAGGG TCTTCCTATG
451  GCCAAGATGA TCTGGCTCTT CTACTTCTCC AAGATCATGG AGTTTGTCGA
501  CACCATGATC ATGGTCCTCA AGAAGAACAA CCGCCAGATC TCCTTCTTGC
551  ACGTTTACCA CCACAGCTCC ATCTTCACCA TCTGGTGGTT GGTCACCTTT
601  GTTGCACCCA ACGGTGAAGC CTACTTCTCT GCTGCGTTGA ACTCGTTCAT
651  CCATGTGATC ATGTACGGCT ACTACTTCTT GTCGGCCTTG GGCTTCAAGC
701  AGGTGTCGTT CATCAAGTTC TACATCACGC GCTCGCAGAT GACACAGTTC
751  TGCATGATGT CGGTCCAGTC TTCCTGGGAC ATGTACGCCA TGAAGGTCCT
801  TGGCCGCCCC GGATACCCCT TCTTCATCAC GGCTCTGCTT TGGTTCTACA
851  TGTGGACCAT GCTCGGTCTC TTCTACAACT TTTACAGAAA GAACGCCAAG
901  TTGGCCAAGC AGGCCAAGGC CGACGCTGCC AAGGAGAAGG CAAGGAAGTT
951  GCAGTAA
```

FIG.22

```
  1  MESIAPFLPS KMPQDLFMDL ATAIGVRAAP YVDPLEAALV AQAEKYIPTI
 51  VHHTRGFLVA VESPLARELP LMNPFHVLLI VLAYLVTVFV GMQIMKNFER
101  FEVKTFSLLH NFCLVSISAY MCGGILYEAY QANYGLFENA ADHTFKGLPM
151  AKMIWLFYFS KIMEFVDTMI MVLKKNNRQI SFLHVYHHSS IFTIWWLVTF
201  VAPNGEAYFS AALNSFIHVI MYGYYFLSAL GFKQVSFIKF YITRSQMTQF
251  CMMSVQSSWD MYAMKVLGRP GYPFFITALL WFYMWTMLGL FYNFYRKNAK
301  LAKQAKADAA KEKARKLQ*
```

FIG.23

Host(plasmid)	334(pRPB2)	334 (pYES2)
Added substrate	25μM GLA	25μM GLA
	(n=4)	
Fatty Acid	% total lipid	
C16:0	15.65	15.23
C16:1	35.2	38.59
C18:0	5.68	5.55
C18:1n-9	25.55	25.27
C18:3n-6	**3.1**	**6.75**
C20:0	0.36	0.14
C20:3n-6	**(62.0%) 5.06**	**(2.6%) 0.18**
Total Lipid (μg)	314	247
(% conversion) = product/(substrate+product)		

FIG.24

Host(plasmid)	334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)
Added substrate	25μM SA	25μM OA	25μM LA	25μM DGLA	25μM AA	25μM Adrenic
	C18:0	C18:1n-9	C18:2n-6	C20:3n-6	C20:4n-6	C22:4n-6
Fatty Acid	% total lipid					
C16:0	15.07	14.52	15.74	15.69	16.06	15.15
C16:1	33.7	32.37	32.23	25.65	33.65	33.39
C18:0	*9.78	5.83	5.61	8.33	4.52	5.35
C18:1n-9	31.2	*37.25	26.05	20.15	24.54	28.54
C18:2n-6			*10.4			
C18:3n-6						
C20:2n-6			0.29			
C20:3n-6				*16.5		
C20:4n-6				0.27	*11.7	
C22:4n-6						*7.46
Total Lipid (μg)	132	130	171	55	225	163

*indicates substrate added

(% conversion) = product/(substrate+product)

FIG.25A

Host(plasmid)	334(pRPB2)	334(pRPB2)	334(pRPB2)
Added substrate	25µM ALA	25µM STA	25µM EPA
	C18:3n-3	C18:4n-3	C20:5n-3
Fatty Acid	% total lipid		
C16:0	17.32	16.01	20.67
C16:1	27.68	34.31	50.7
C18:0	6.75	5.39	6.14
C18:1n-9	28.4	28.54	
C18:3n-3	*8.39		
C18:4n-3		*1.95	
C20:4n-3		(73.2%) 5.33	
C20:5n-3			*10.33
C22:5n-3			0.25
Total Lipid (µg)	114	199	201

*indicates substrate added
(% conversion) = product/(substrate+product)

FIG.25B

Host(plasmid)	334(pRPB2+PRPE31)	334(pYES2+pYX242)
Added substrate	25μM GLA	25μM GLA
Fatty Acid	% total lipid	
C16:0	15.54	18.26
C16:1	30.16	33.51
C18:0	8.76	5.58
C18:1n-9	27	27.37
C18:3n-6	*2.6	*5.6
C20:0	0.4	0.32
C20:3n-6	**(57.4%) 3.55**	**(2.9%) 0.17**
C20:4n-6	**(27.6%) 1.32**	**ND**
Total Lipid (μg)	254	258

* indicates substrate added
(% conversion) = product/(substrate+product)

FIG. 26A

Host(plasmid)	334(pRPB2+PRPE31)	334(pYES2+pYX242)
Added substrate	25μM STA	25μM STA
Fatty Acid	% total lipid	
C16:0	18	16.4
C16:1	28.37	34.78
C18:0	7.42	5.71
C18:1n-9	26.44	30.15
C18:4n-3	*2.93	*4.57
C20:0	0.25	0.17
C20:4n-3	4.13	0.32
C20:5n-3	**(39%) 1.87**	**(2.1%) .10**
Total Lipid (μg)	257	304

* indicates substrate added
(% conversion) = product/(substrate+product)

FIG. 26B

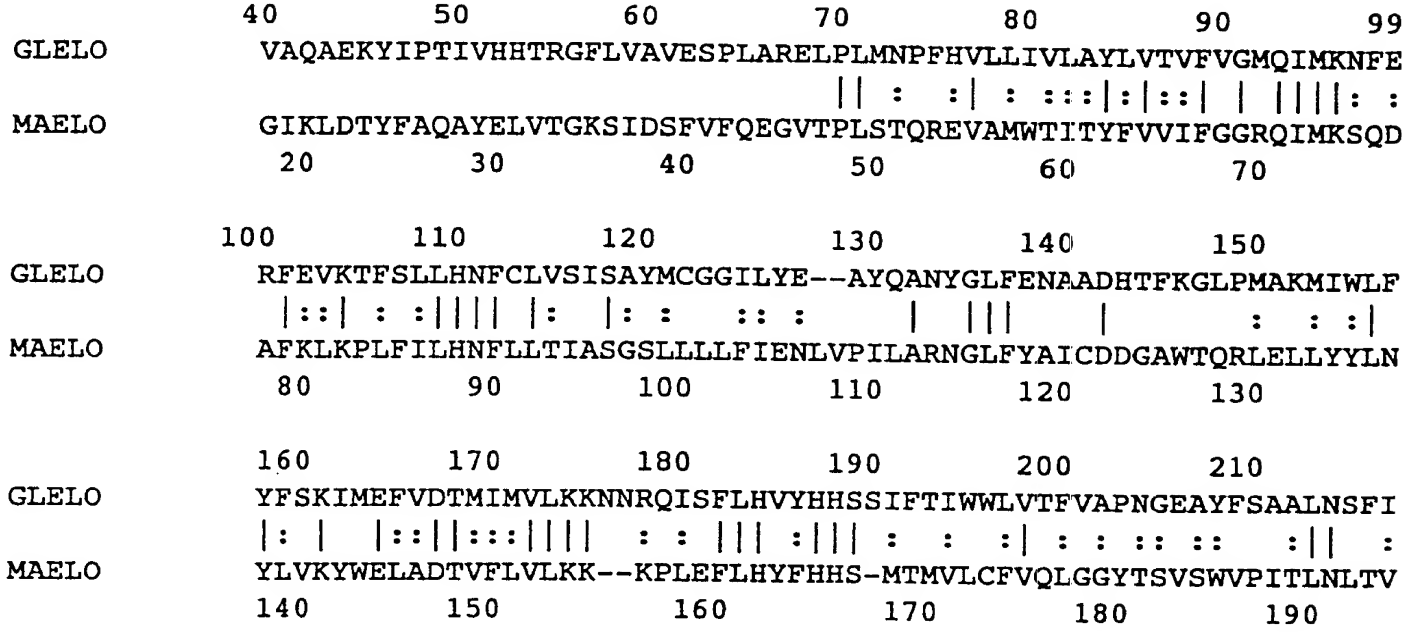
40 50 60 70 80 90 99
GLELO VAQAEKYIPTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYLVTVFVGMQIMKNFE
MAELO GIKLDTYFAQAYELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQD
20 30 40 50 60 70
100 110 120 130 140 150
GLELO RFEVKTFSLLHNFCLVSISAYMCGGILYE--AYQANYGLFENAADHTFKGLPMAKMIWLF
MAELO AFKLKPLFILHNFLLTIASGSLLLLFIENLVPILARNGLFYAICDDGAWTQRLELLYYLN
80 90 100 110 120 130
160 170 180 190 200 210
GLELO YFSKIMEFVDTMIMVLKKNNRQISFLHVYHHSSIFTIWWLVTFVAPNGEAYFSAALNSFI
MAELO YLVKYWELADTVFLVLKK--KPLEFLHYFHHS-MTMVLCFVQLGGYTSVSWVPITLNLTV
140 150 160 170 180 190

FIG. 27A

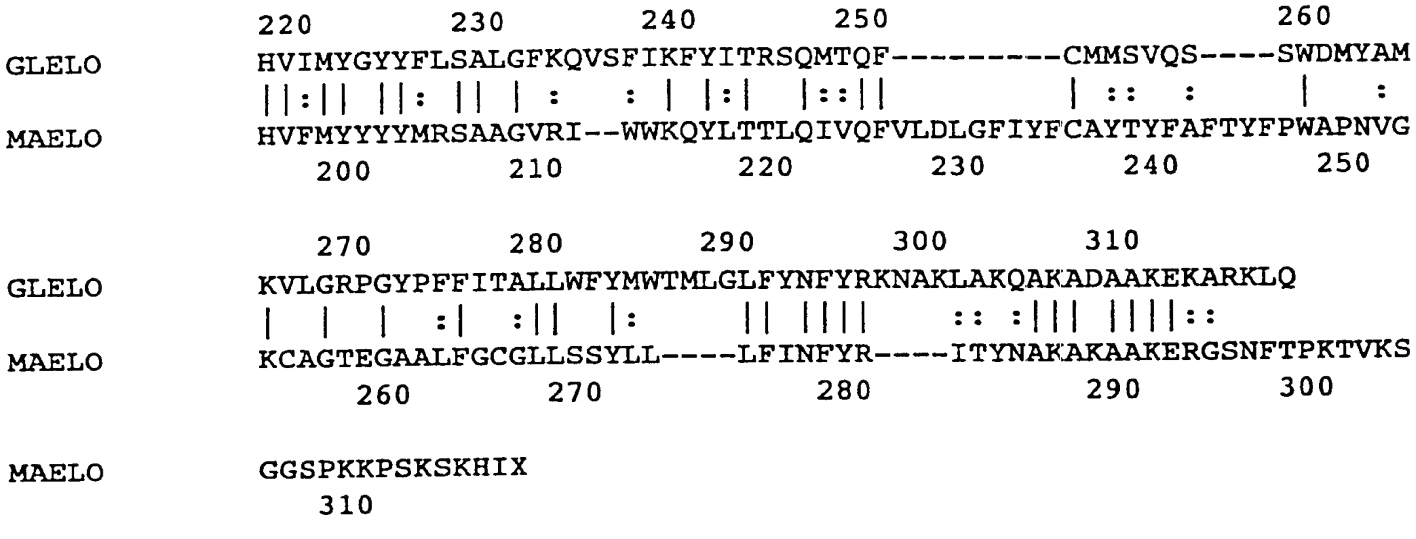
220 230 240 250 260
GLELO HVIMYGYYFLSALGFKQVSFIKFYITRSQMTQF---------CMMSVQS----SWDMYAM
MAELO HVFMYYYYMRSAAGVRI--WWKQYLTTLQIVQFVLDLGFIYFCAYTYFAFTYFPWAPNVG
200 210 220 230 240 250
270 280 290 300 310
GLELO KVLGRPGYPFFITALLWFYMWTMLGLFYNFYRKNAKLAKQAKADAAKEKARKLQ
MAELO KCAGTEGAALFGCGLLSSYLL----LFINFYR----ITYNAKAKAAKERGSNFTPKTVKS
260 270 280 290 300
MAELO GGSPKKPSKSKHIX
310

FIG. 27B

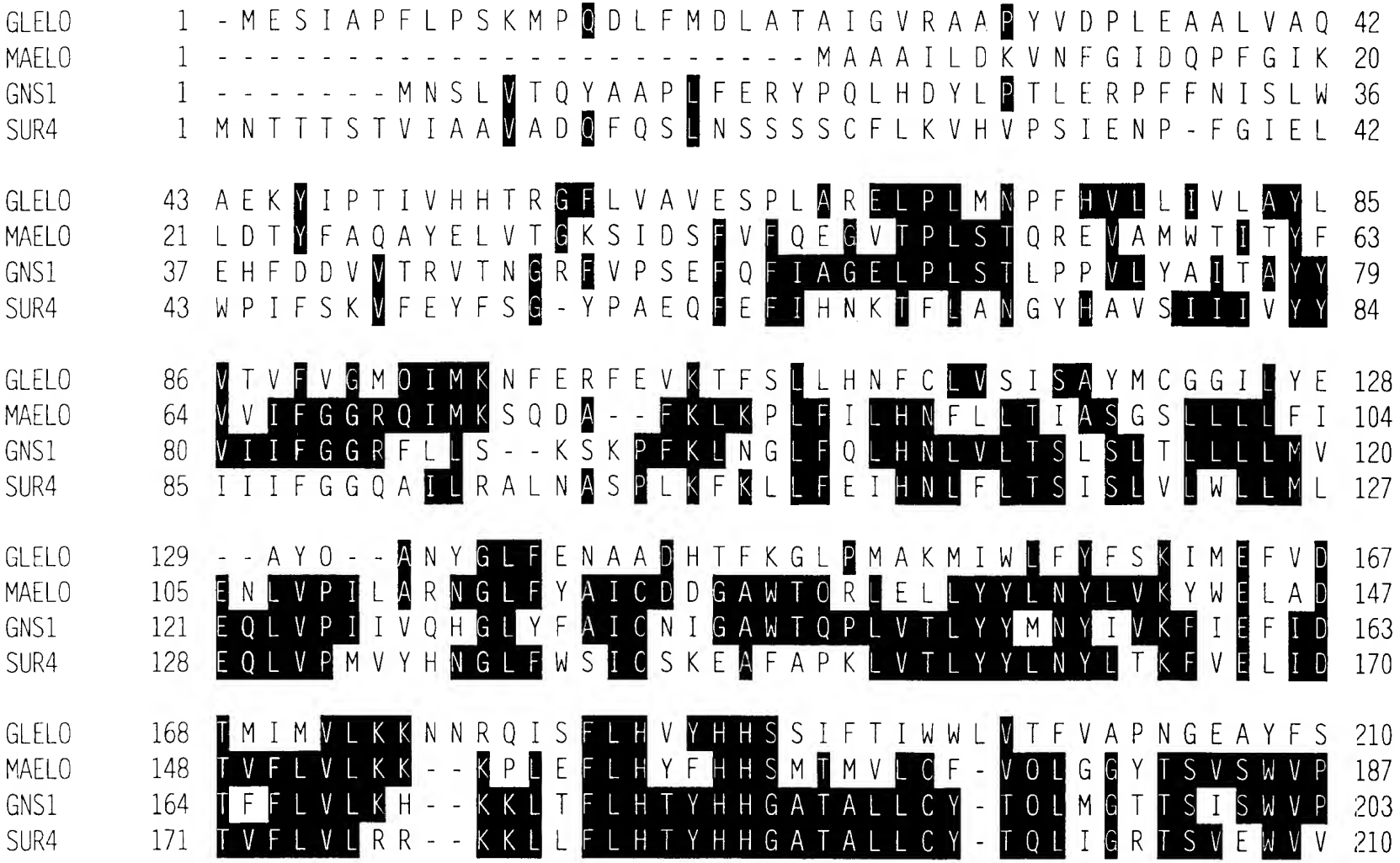
GLELO 1 -MESIAPFLPSKMPQDLFMDLATAIGVRAAPYVDPLEAALVAQ 42
MAELO 1 ----------MAAAILDKVNFGIDQPFGIK 20
GNS1 1 -------MNSLVTQYAAPLFERYPQLHDYLPTLERPFFNISLW 36
SUR4 1 MNTTTSTVIAAVADQFQSLNSSSSSCFLKVHVPSIENP-FGIEL 42
GLELO 43 AEKYIPTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYL 85
MAELO 21 LDTYFAQAYELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYF 63
GNS1 37 EHFDDVVTRVTNGRFVPSEFQFIAGELPLSTLPPVLYAITAYY 79
SUR4 43 WPIFSKVFEYFSG-YPAEQFEFIHNKTFLANGYHAVSIIIVYY 84
GLELO 86 VTVFVGMQIMKNFERFEVKTFSLLHNFCLVSISAYMCGGILYE 128
MAELO 64 VVIFGGRQIMKSQDA--FKLKPLFILHNFLLTIASGSLLLLFI 104
GNS1 80 VIIFGGRFLLS--KSKPFKLNGLFQLHNLVLTSLSLTLLLLMV 120
SUR4 85 IIIFGGQAILRALNASPLKFKLLFEIHNLFLTSISLVLWLLML 127
GLELO 129 --AYQ--ANYGLFENAADHTFKGLPMAKMIWLFYFSKIMEFVD 167
MAELO 105 ENLVPILARNGLFYAICDDGAWTQRLELLYYLNYLVKYWELAD 147
GNS1 121 EQLVPIIVQHGLYFAICNIGAWTQPLVTLYYMNYIVKFIEFID 163
SUR4 128 EQLVPMVYHNGLFWSICSKEAFAPKLVTLYYLNYLTKFVELID 170
GLELO 168 TMIMVLKKNNRQISFLHVYHHSSIFTIWWLVTFVAPNGEAYFS 210
MAELO 148 TVFLVLKK--KPLEFLHYFHHSMTMVLCF-VQLGGYTSVSWVP 187
GNS1 164 TFFLVLKH--KKLTFLHTYHHGATALLCY-TQLMGTTSISWVP 203
SUR4 171 TVFLVLRR--KKLLFLHTYHHGATALLCY-TQLIGRTSVEWVV 210

FIG.28A

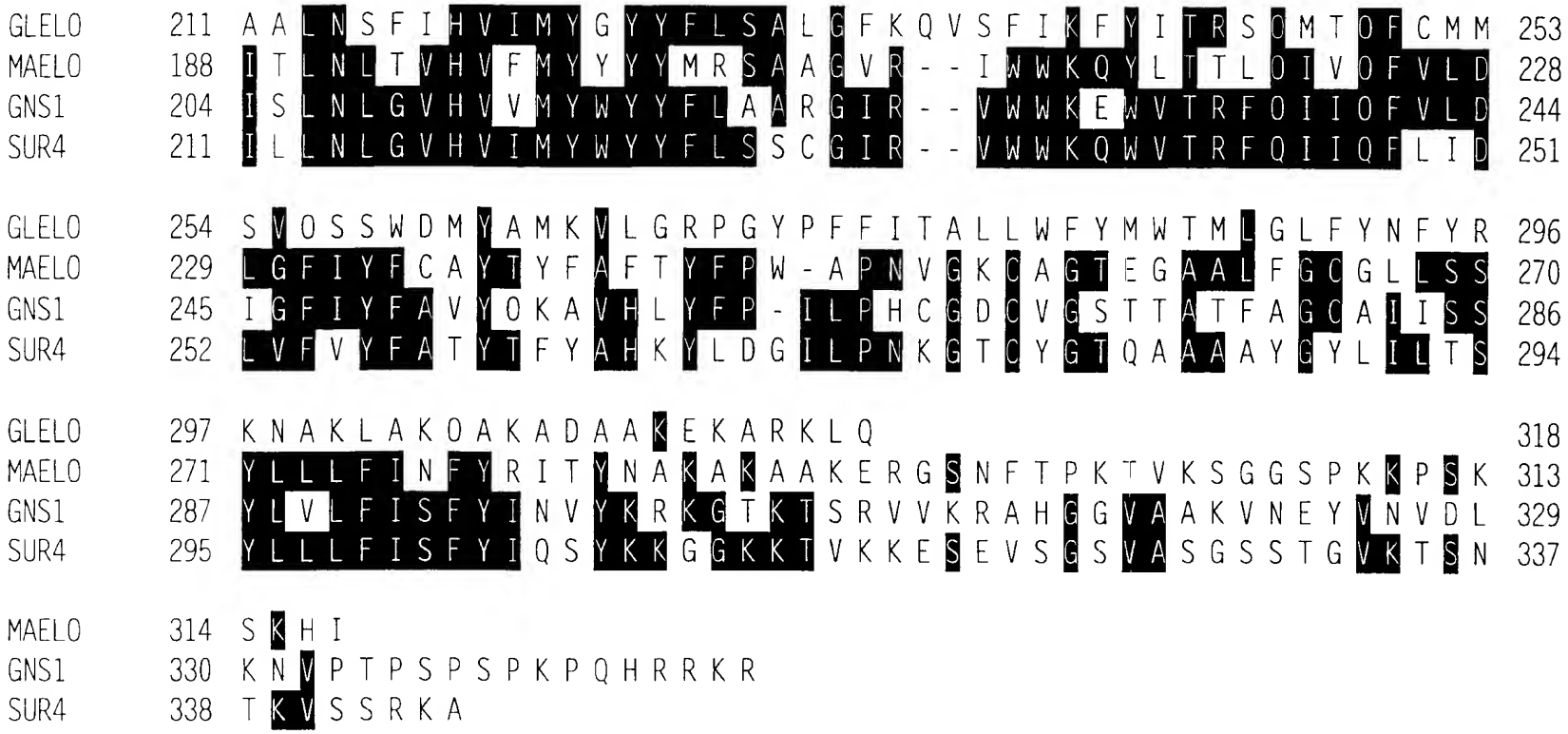
GLELO 211 AALNSFIHVIMYGYYFLSALGFKQVSFIKFYITRSQMTQFCMM 253
MAELO 188 ITLNLTVHVFMYYYYMRSAAGVR--IWWKQYLTTLQIVQFVLD 228
GNS1 204 ISLNLGVHVVMYWYYFLAARGIR--VWWKEWVTRFQIIQFVLD 244
SUR4 211 ILLNLGVHVIMYWYYFLSSCGIR--VWWKQWVTRFQIIQFLID 251
GLELO 254 SVQSSWDMYAMKVLGRPGYPFFITALLWFYMWTMLGLFYNFYR 296
MAELO 229 LGFIYFCAYTYFAFTYFPW-APNVGKCAGTEGAALFGCGLLSS 270
GNS1 245 IGFIYFAVYQKAVHLYFP-ILPHCGDCVGSTTATFAGCAIISS 286
SUR4 252 LVFVYFATYTFYAHKYLDGILPNKGTCYGTQAAAAYGYLILTS 294
GLELO 297 KNAKLAKQAKADAAKEKARKLQ 318
MAELO 271 YLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSK 313
GNS1 287 YLVLFISFYINVYKRKGTKTSRVVKRAHGGVAAKVNEYVNVDL 329
SUR4 295 YLLLFISFYIQSYKKGGKKTVKKESEVSGSVASGSSTGVKTSN 337
MAELO 314 SKHI
GNS1 330 KNVPTPSPSPKPQHRRKR
SUR4 338 TKVSSRKA

FIG.28B

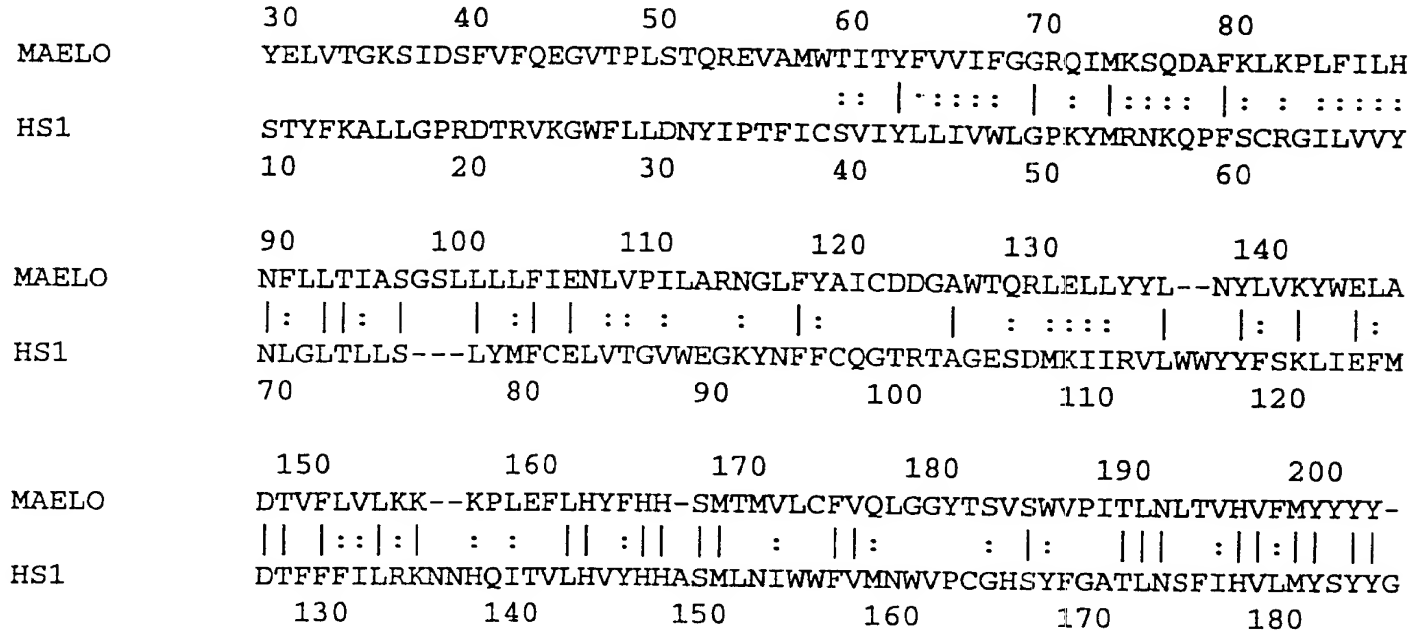
30 40 50 60 70 80
MAELO YELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFILH
HS1 STYFKALLGPRDTRVKGWFLLDNYIPTFICSVIYLLIVWLGPKYMRNKQPFSCRGILVVY
10 20 30 40 50 60
90 100 110 120 130 140
MAELO NFLLTIASGSLLLLFIENLVPILARNGLFYAICDDGAWTQRLELLYYL--NYLVKYWELA
HS1 NLGLTLLS---LYMFCELVTGVWEGKYNFFCQGTRTAGESDMKIIRVLWWYYFSKLIEFM
70 80 90 100 110 120
150 160 170 180 190 200
MAELO DTVFLVLKK--KPLEFLHYFHH-SMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYY-
HS1 DTFFFILRKNNHQITVLHVYHHASMLNIWWFVMNWVPCGHSYFGATLNSFIHVLMYSYYG
130 140 150 160 170 180

FIG. 29A

```
                 210         220         230         240         250         260
MAELO       MRSAAGVR--IWWKQYLTTLQIVQFVLDLGFIYFCAYTYFAFTYFPWAPNVGKCAGTEGA
            : |: ::|  :|||:|:|  |::|||| : :   |:          | |    |:   |
HS1         LSSVPSMRPYLWWKKYITQGQLLQFVLTI-IQTSCGVI--------W-P----CTFPLGW
              190       200       210       220                   230

                   270       280       290       300       310
MAELO       ALFGCGLLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHI
              |  | : | : || |||  ||| |: : ::
HS1         LYFQIGYMISLIALFTNFYIQTYNKKGASRRKDHLKDHQNGSMAAVNGHTNSFSPLENNV
                  240       250       260       270       280       290

HS1         KPRKLRKDX
                  300
```

FIG. 29B

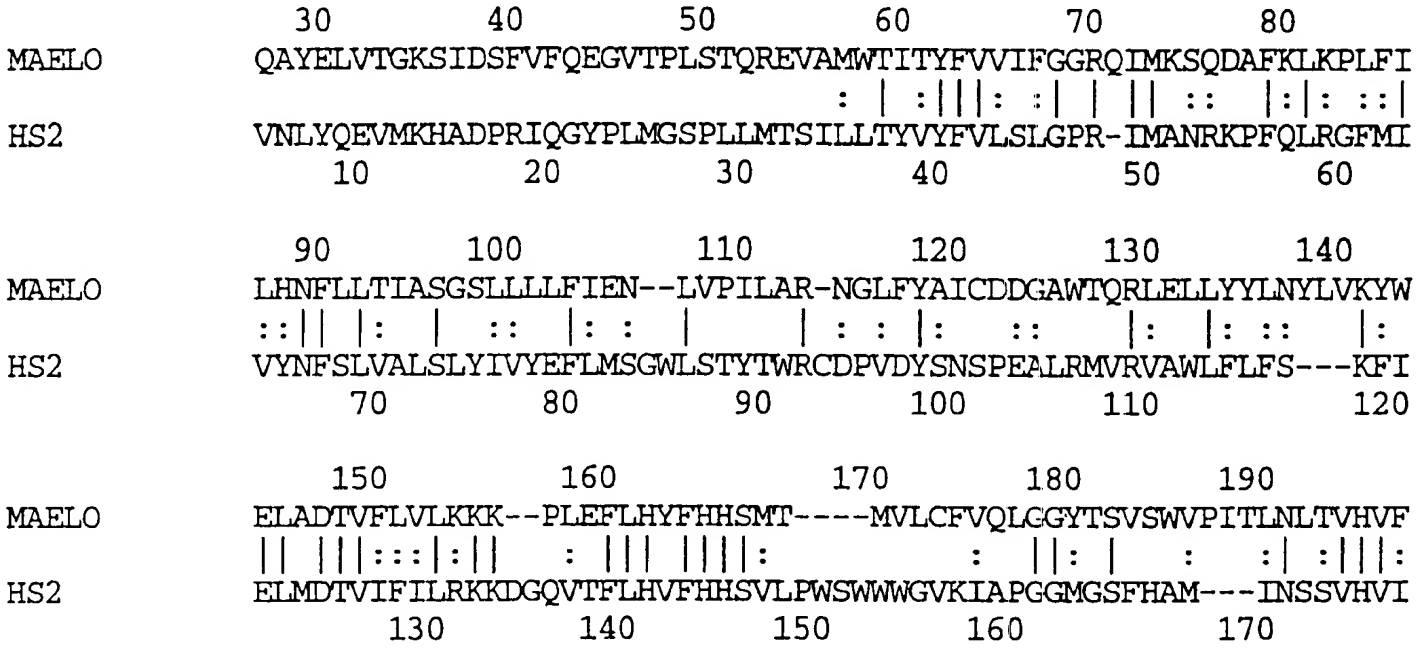
30 40 50 60 70 80
MAELO QAYELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFI
HS2 VNLYQEVMKHADPRIQGYPLMGSPLLMTSILLTYVYFVLSLGPR-IMANRKPFQLRGFMI
10 20 30 40 50 60
90 100 110 120 130 140
MAELO LHNFLLTIASGSLLLLFIEN--LVPILAR-NGLFYAICDDGAWTQRLELLYYLNYLVKYW
HS2 VYNFSLVALSLYIVYEFLMSGWLSTYTWRCDPVDYSNSPEALRMVRVAWLFLFS---KFI
70 80 90 100 110 120
150 160 170 180 190
MAELO ELADTVFLVLKKK--PLEFLHYFHHSMT----MVLCFVQLGGYTSVSWVPITLNLTVHVF
HS2 ELMDTVIFILRKKDGQVTFLHVFHHSVLPWSWWWGVKIAPGGMGSFHAM---INSSVHVI
130 140 150 160 170

FIG. 30A

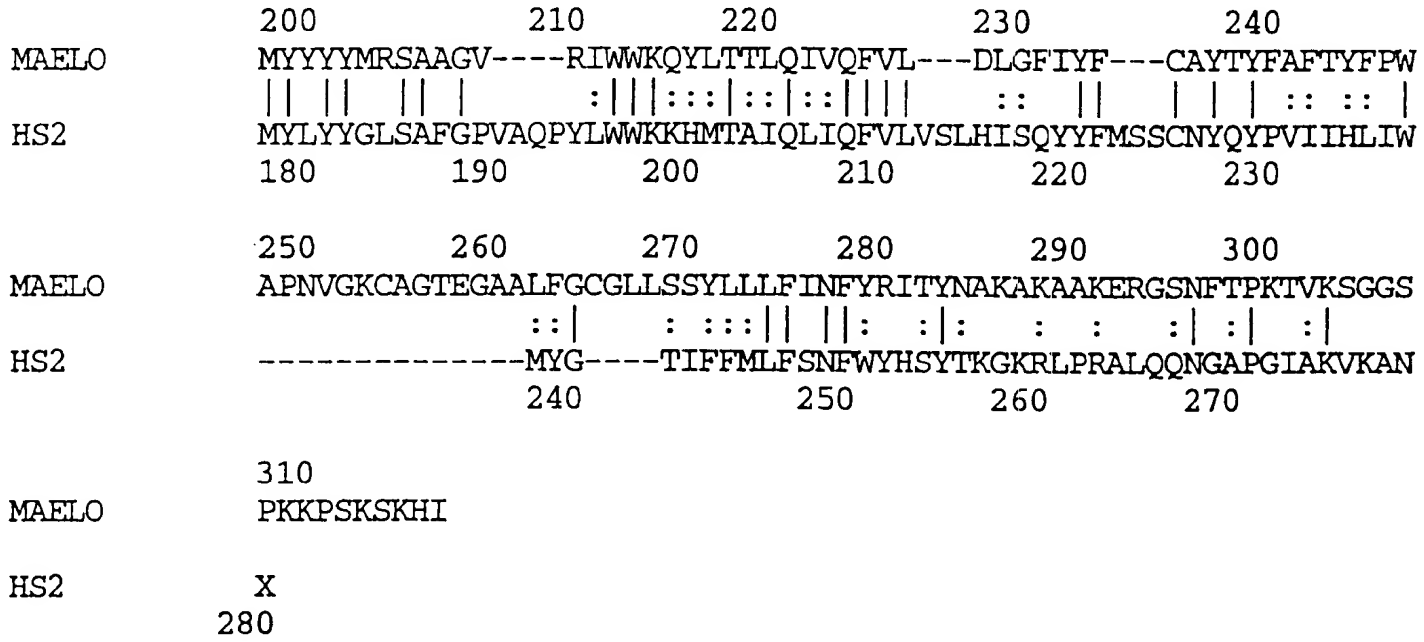
200 210 220 230 240
MAELO MYYYYMRSAAGV----RIWWKQYLTTLQIVQFVL---DLGFIYF---CAYTYFAFTYFPW
HS2 MYLYYGLSAFGPVAQPYLWWKKHMTAIQLIQFVLVSLHISQYYFMSSCNYQYPVIIHLIW
180 190 200 210 220 230
250 260 270 280 290 300
MAELO APNVGKCAGTEGAALFGCGLLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGS
HS2 ----------MYG----TIFFMLFSNFWYHSYTKGKRLPRALQQNGAPGIAKVKAN
240 250 260 270
310
MAELO PKKPSKSKHI
HS2 X
280

FIG. 30B

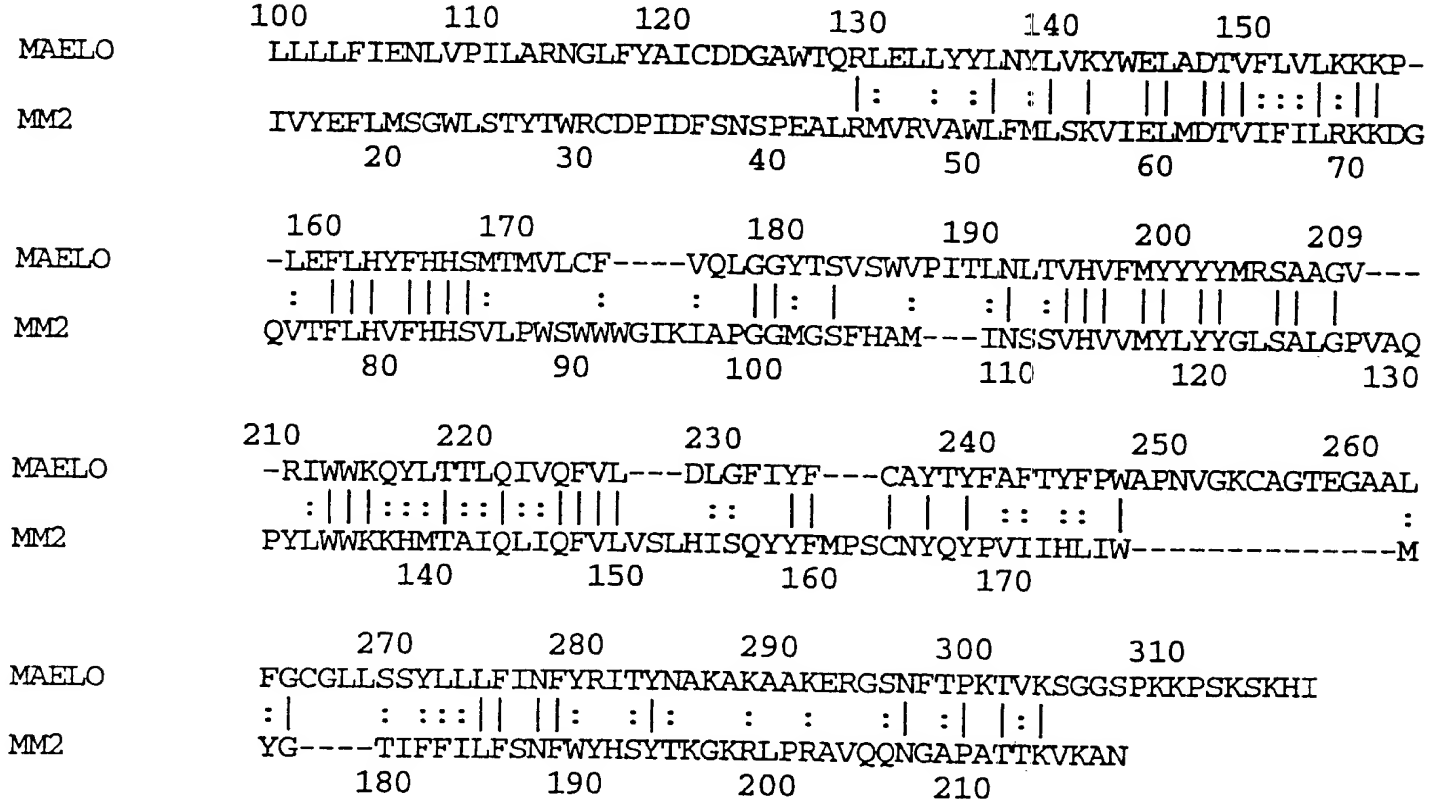
100 110 120 130 140 150
MAELO LLLLFIENLVPILARNGLFYAICDDGAWTQRLELLYYLNYLVKYWELADTVFLVLKKKP-
MM2 IVYEFLMSGWLSTYTWRCDPIDFSNSPEALRMVRVAWLFMLSKVIELMDTVIFILRKKDG
20 30 40 50 60 70
160 170 180 190 200 209
MAELO -LEFLHYFHHSMTMVLCF----VQLGGYTSVSWVPITLNLTVHVFMYYYYMRSAAGV---
MM2 QVTFLHVFHHSVLPWSWWWGIKIAPGGMGSFHAM---INSSVHVVMYLYYGLSALGPVAQ
80 90 100 110 120 130
210 220 230 240 250 260
MAELO -RIWWKQYLTTLQIVQFVL---DLGFIYF---CAYTYFAFTYFPWAPNVGKCAGTEGAAL
MM2 PYLWWKKHMTAIQLIQFVLVSLHISQYYFMPSCNYQYPVIIHLIW----------M
140 150 160 170
270 280 290 300 310
MAELO FGCGLLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHI
MM2 YG----TIFFILFSNFWYHSYTKGKRLPRAVQQNGAPATTKVKAN
180 190 200 210

FIG.31

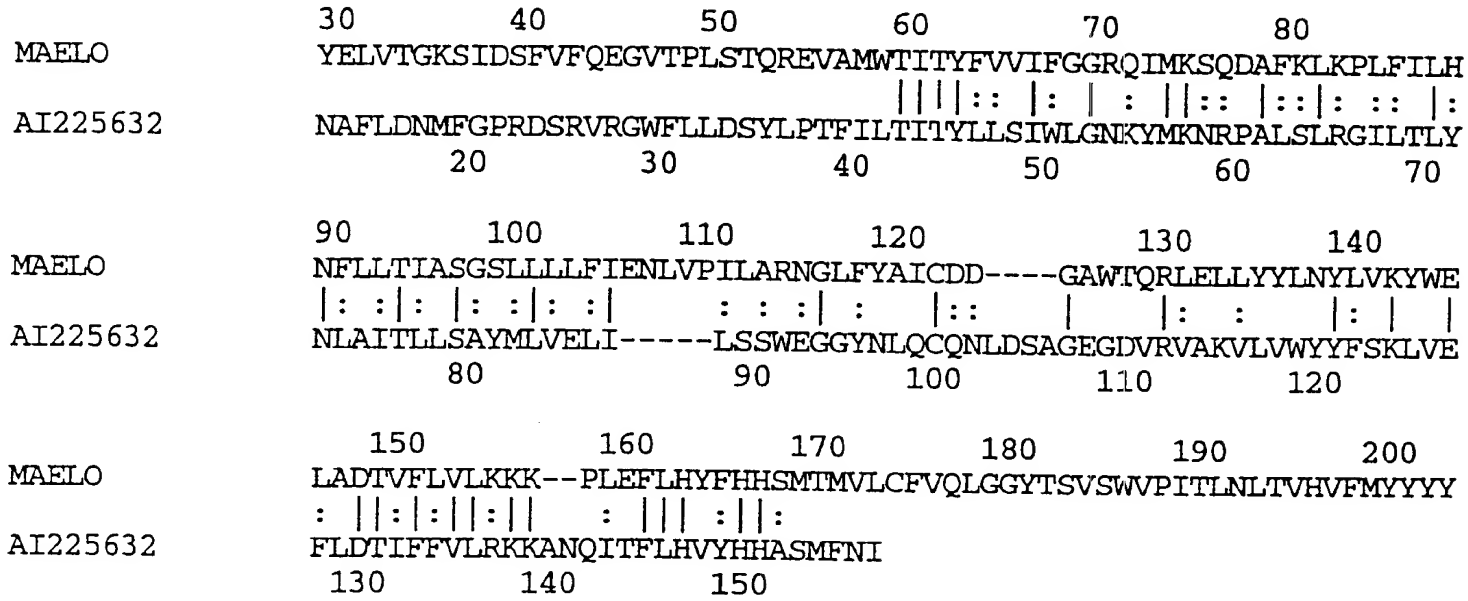
30 40 50 60 70 80
MAELO YELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFILH
AI225632 NAFLDNMFGPRDSRVRGWFLLDSYLPTFILTITYLLSIWLGNKYMKNRPALSLRGILTLY
20 30 40 50 60 70
90 100 110 120 130 140
MAELO NFLLTIASGSLLLLFIENLVPILARNGLFYAICDD----GAWTQRLELLYYLNYLVKYWE
AI225632 NLAITLLSAYMLVELI-----LSSWEGGYNLQCQNLDSAGEGDVRVAKVLVWYYFSKLVE
80 90 100 110 120
150 160 170 180 190 200
MAELO LADIVFLVLKKK--PLEFLHYFHHSMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYY
AI225632 FLDTIFFVLRKKANQITFLHVYHHASMFNI
130 140 150

FIG.32

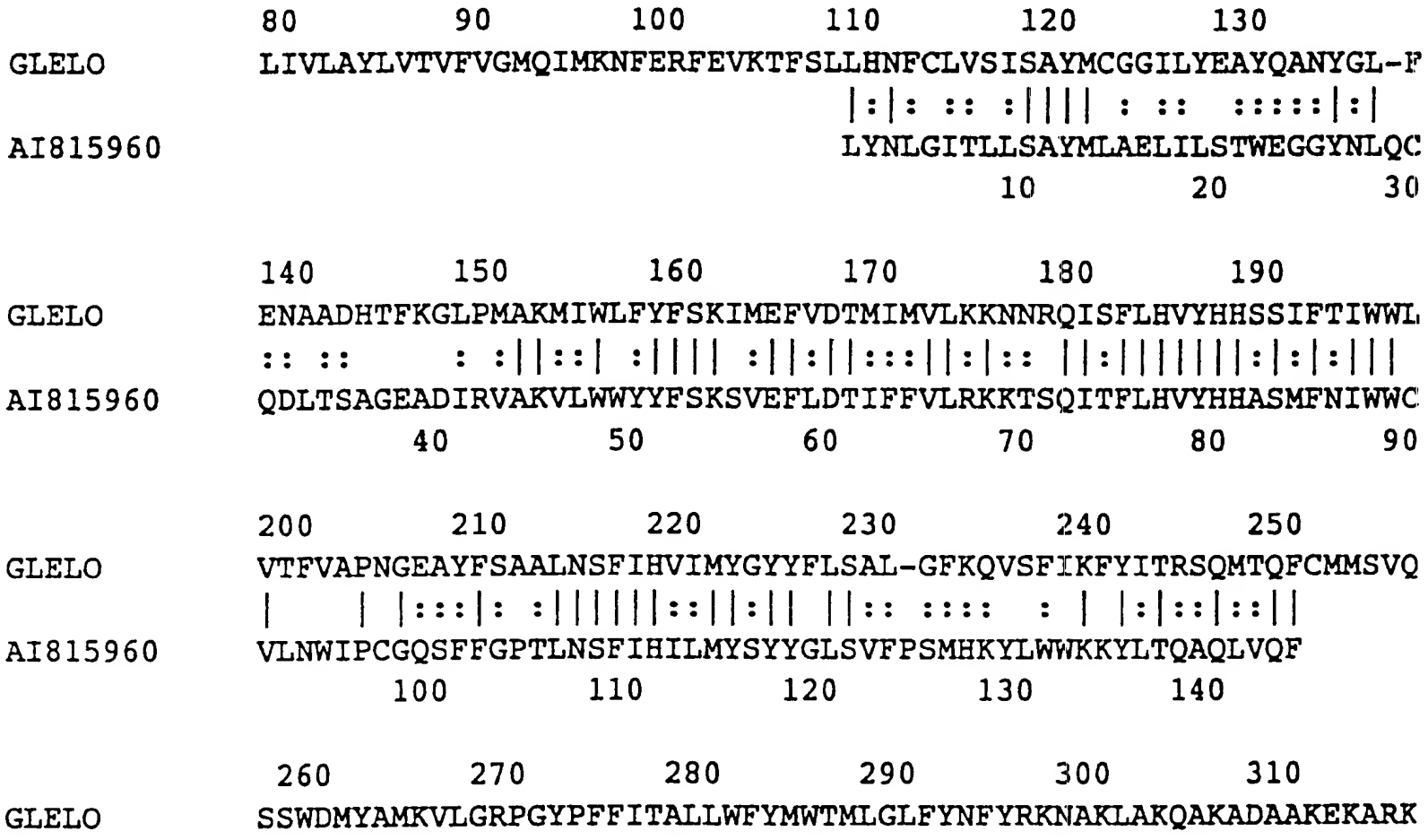
80 90 100 110 120 130
GLELO LIVLAYLVTVFVGMQIMKNFERFEVKTFSLLHNFCLVSISAYMCGGILYEAYQANYGL-F
AI815960 LYNLGITLLSAYMLAELILSTWEGGYNLQC
10 20 30
140 150 160 170 180 190
GLELO ENAADHTFKGLPMAKMIWLFYFSKIMEFVDTMIMVLKKNNRQISFLHVYHHSSIFTIWWL
AI815960 QDLTSAGEADIRVAKVLWWYYFSKSVEFLDTIFFVLRKKTSQITFLHVYHHASMFNIWWC
40 50 60 70 80 90
200 210 220 230 240 250
GLELO VTFVAPNGEAYFSAALNSFIHVIMYGYYFLSAL-GFKQVSFIKFYITRSQMTQFCMMSVQ
AI815960 VLNWIPCGQSFFGPTLNSFIHILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQF
100 110 120 130 140
260 270 280 290 300 310
GLELO SSWDMYAMKVLGRPGYPFFITALLWFYMWTMLGLFYNFYRKNAKLAKQAKADAAKEKARK

FIG.33

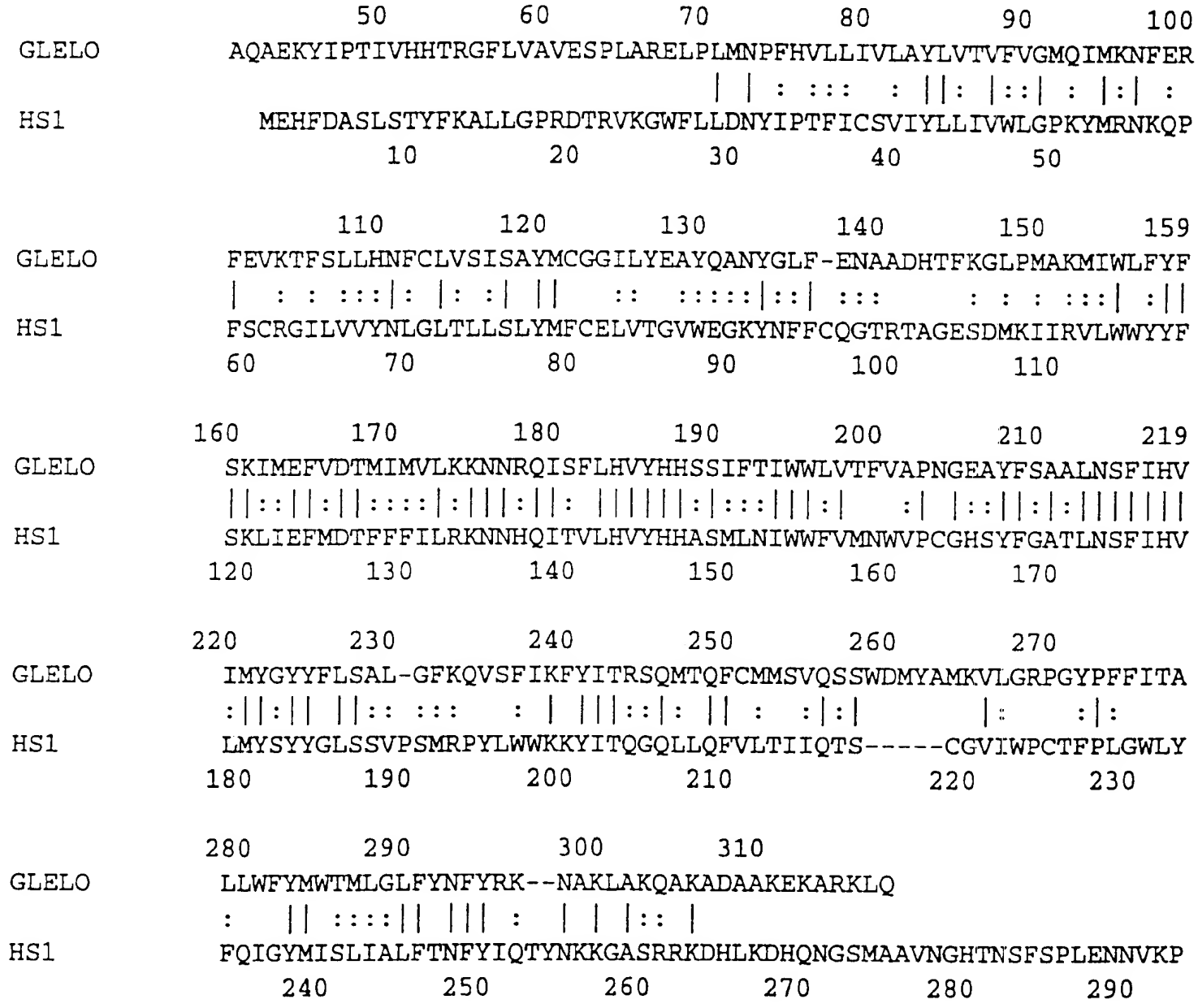
50 60 70 80 90 100
GLELO AQAEKYIPTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYLVTVFVGMQIMKNFER
HS1 MEHFDASLSTYFKALLGPRDTRVKGWFLLDNYIPTFICSVIYLLIVWLGPKYMRNKQP
10 20 30 40 50
110 120 130 140 150 159
GLELO FEVKTFSLLHNFCLVSISAYMCGGILYEAYQANYGLF-ENAADHTFKGLPMAKMIWLFYF
HS1 FSCRGILVVYNLGLTLLSLYMFCELVTGVWEGKYNFFCQGTRTAGESDMKIIRVLWWYYF
60 70 80 90 100 110
160 170 180 190 200 210 219
GLELO SKIMEFVDTMIMVLKKNNRQISFLHVYHHSSIFTIWWLVTFVAPNGEAYFSAALNSFIHV
HS1 SKLIEFMDTFFFILRKNNHQITVLHVYHHASMLNIWWFVMNWVPCGHSYFGATLNSFIHV
120 130 140 150 160 170
220 230 240 250 260 270
GLELO IMYGYYFLSAL-GFKQVSFIKFYITRSQMTQFCMMSVQSSWDMYAMKVLGRPGYPFFITA
HS1 LMYSYYGLSSVPSMRPYLWWKKYITQGQLLQFVLTIIQTS-----CGVIWPCTFPLGWLY
180 190 200 210 220 230
280 290 300 310
GLELO LLWFYMWTMLGLFYNFYRK--NAKLAKQAKADAAKEKARKLQ
HS1 FQIGYMISLIALFTNFYIQTYNKKGASRRKDHLKDHQNGSMAAVNGHTNSFSPLENNVKP
240 250 260 270 280 290

FIG.34

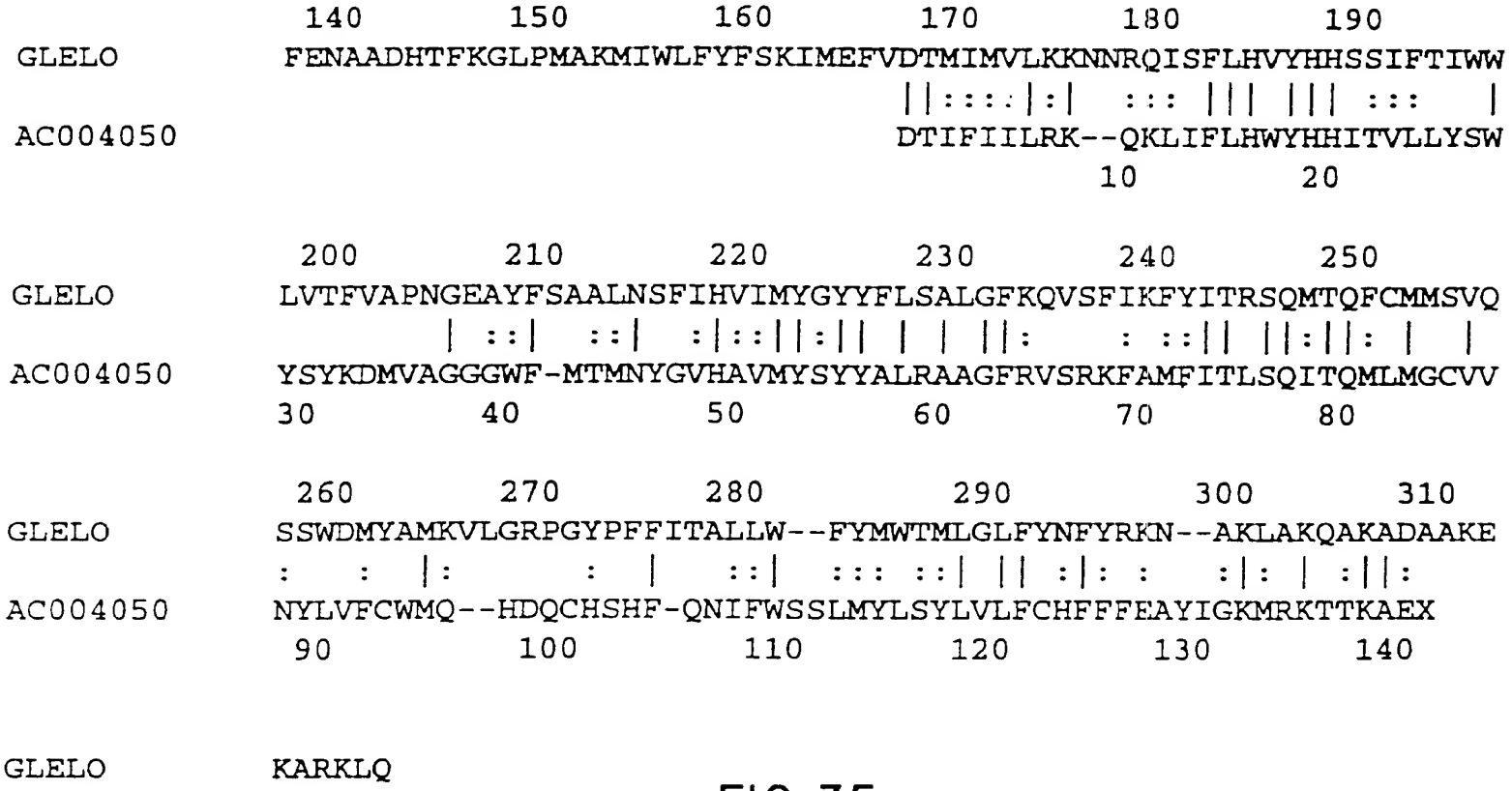
140 150 160 170 180 190
GLELO FENAADHTFKGLPMAKMIWLFYFSKIMEFVDTMIMVLKKNNRQISFLHVYHHSSIFTIWW
AC004050 DTIFIILRK--QKLIFLHWYHHITVLLYSW
10 20
200 210 220 230 240 250
GLELO LVTFVAPNGEAYFSAALNSFIHVIMYGYYFLSALGFKQVSFIKFYITRSQMTQFCMMSVQ
AC004050 YSYKDMVAGGGWF-MTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSQITQMLMGCVV
30 40 50 60 70 80
260 270 280 290 300 310
GLELO SSWDMYAMKVLGRPGYPFFITALLW--FYMWTMLGLFYNFYRKN--AKLAKQAKADAAKE
AC004050 NYLVFCWMQ--HDQCHSHF-QNIFWSSLMYLSYLVLFCHFFFEAYIGKMRKTTKAEX
90 100 110 120 130 140
GLELO KARKLQ

FIG.35

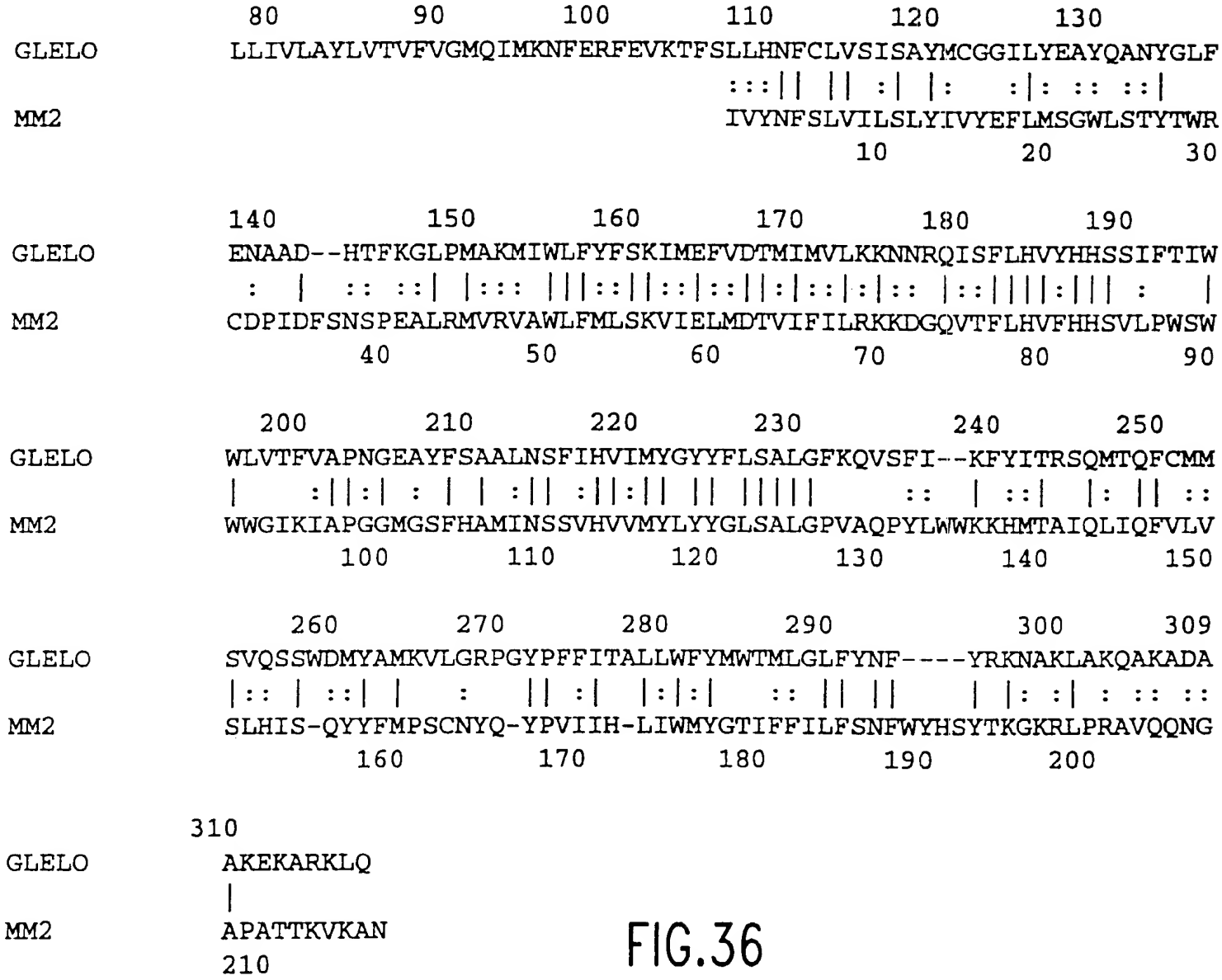
80 90 100 110 120 130
GLELO LLIVLAYLVTVFVGMQIMKNFERFEVKTFSLLHNFCLVSISAYMCGGILYEAYQANYGLF
MM2 IVYNFSLVILSLYIVYEFLMSGWLSTYTWR
10 20 30
140 150 160 170 180 190
GLELO ENAAD--HTFKGLPMAKMIWLFYFSKIMEFVDTMIMVLKKNNRQISFLHVYHHSSIFTIW
MM2 CDPIDFSNSPEALRMVRVAWLFMLSKVIELMDTVIFILRKKDGQVTFLHVFHHSVLPWSW
40 50 60 70 80 90
200 210 220 230 240 250
GLELO WLVTFVAPNGEAYFSAALNSFIHVIMYGYYFLSALGFKQVSFI--KFYITRSQMTQFCMM
MM2 WWGIKIAPGGMGSFHAMINSSVHVVMYLYYGLSALGPVAQPYLWWKKHMTAIQLIQFVLV
100 110 120 130 140 150
260 270 280 290 300 309
GLELO SVQSSWDMYAMKVLGRPGYPFFITALLWFYMWTMLGLFYNF----YRKNAKLAKQAKADA
MM2 SLHIS-QYYFMPSCNYQ-YPVIIH-LIWMYGTIFFILFSNFWYHSYTKGKRLPRAVQQNG
160 170 180 190 200
310
GLELO AKEKARKLQ
MM2 APATTKVKAN
210

FIG.36

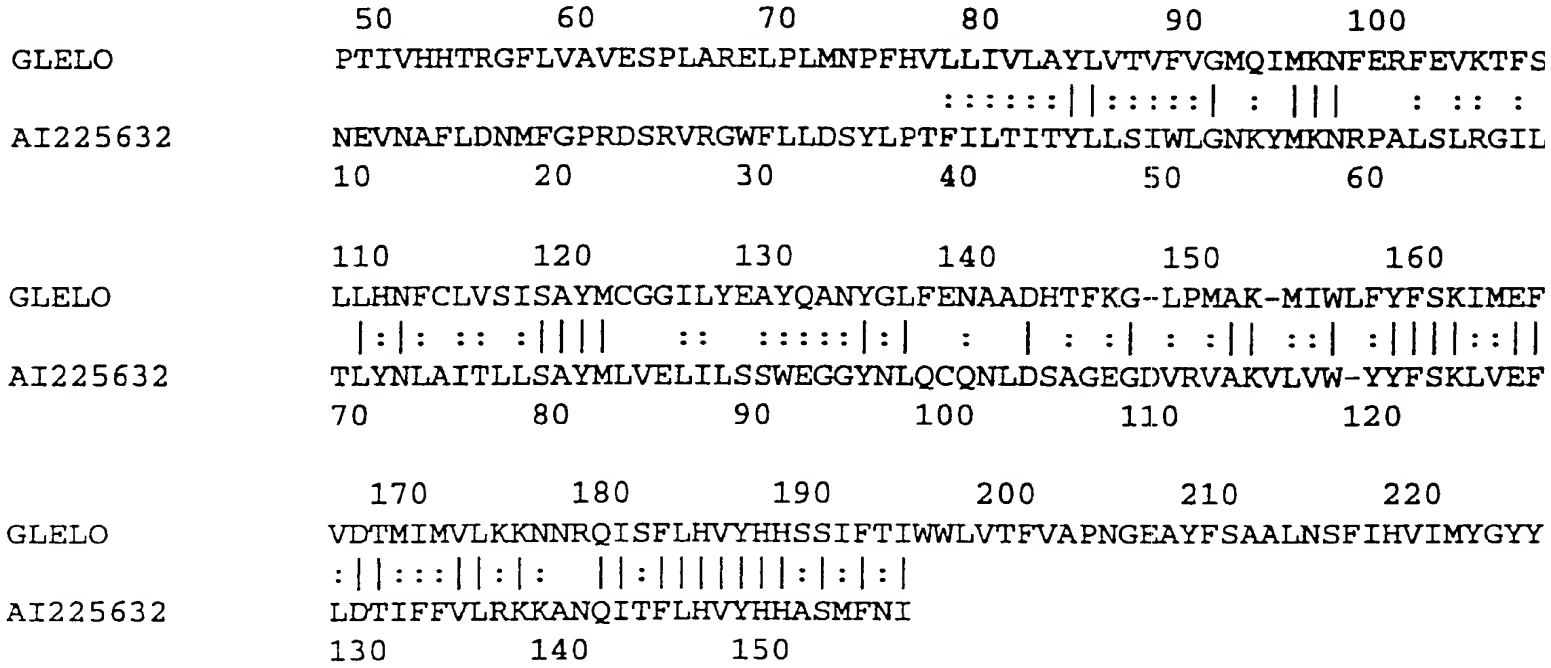
50 60 70 80 90 100
GLELO PTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYLVTVFVGMQIMKNFERFEVKTFS
AI225632 NEVNAFLDNMFGPRDSRVRGWFLLDSYLPTFILTITYLLSIWLGNKYMKNRPALSLRGIL
10 20 30 40 50 60
110 120 130 140 150 160
GLELO LLHNFCLVSISAYMCGGILYEAYQANYGLFENAADHTFKG--LPMAK-MIWLFYFSKIMEF
AI225632 TLYNLAITLLSAYMLVELILSSWEGGYNLQCQNLDSAGEGDVRVAKVLVW-YYFSKLVEF
70 80 90 100 110 120
170 180 190 200 210 220
GLELO VDTMIMVLKKNNRQISFLHVYHHSSIFTIWWLVTFVAPNGEAYFSAALNSFIHVIMYGYY
AI225632 LDTIFFVLRKKANQITFLHVYHHASMFNI
130 140 150

FIG.37

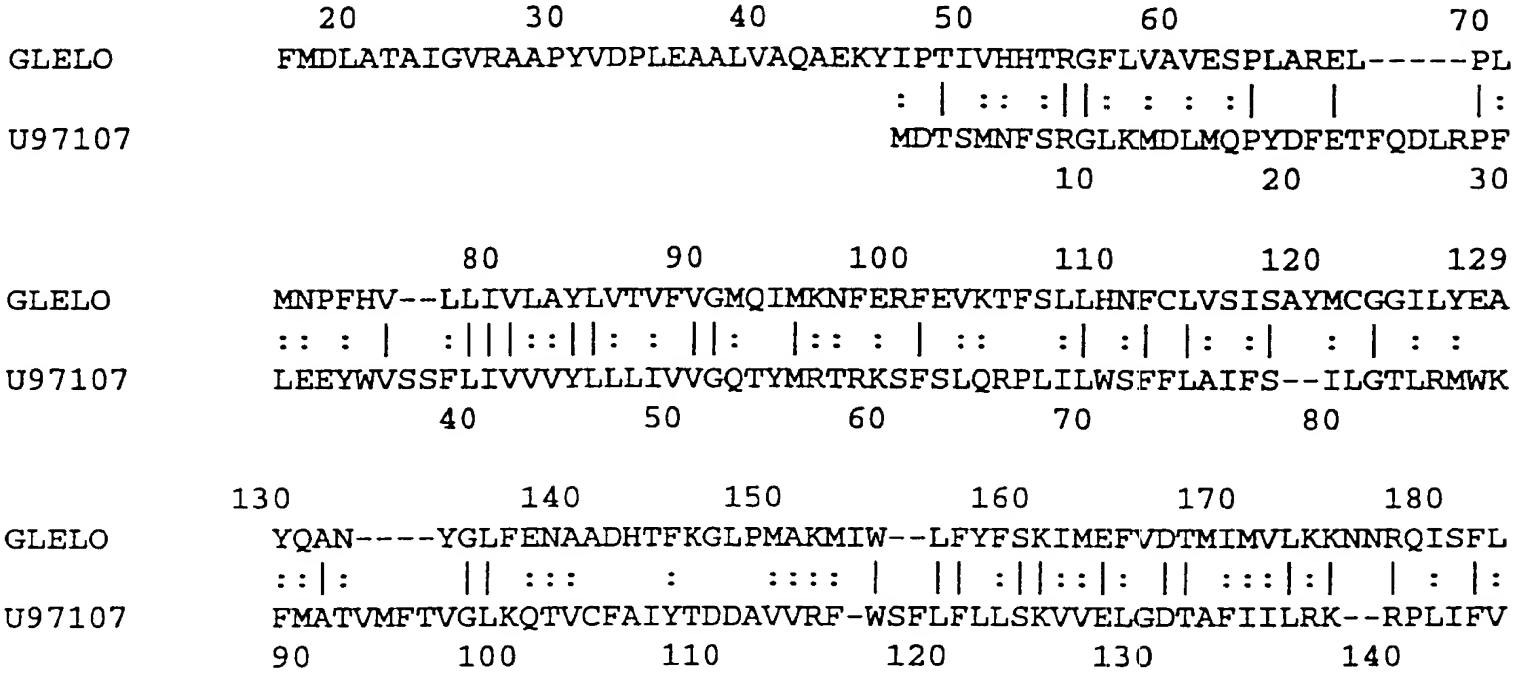
20 30 40 50 60 70
GLELO FMDLATAIGVRAAPYVDPLEAALVAQAEKYIPTIVHHTRGFLVAVESPLAREL-----PL
U97107 MDTSMNFSRGLKMDLMQPYDFETFQDLRPF
10 20 30
80 90 100 110 120 129
GLELO MNPFHV--LLIVLAYLVTVFVGMQIMKNFERFEVKTFSLLHNFCLVSISAYMCGGILYEA
U97107 LEEYWVSSFLIVVVYLLLIVVGQTYMRTRKSFSLQRPLILWSFFLAIFS--ILGTLRMWK
40 50 60 70 80
130 140 150 160 170 180
GLELO YQAN----YGLFENAADHTFKGLPMAKMIW--LFYFSKIMEFVDTMIMVLKKNNRQISFL
U97107 FMATVMFTVGLKQTVCFAIYTDDAVVRF-WSFLFLLSKVVELGDTAFIILRK--RPLIFV
90 100 110 120 130 140

FIG.38A

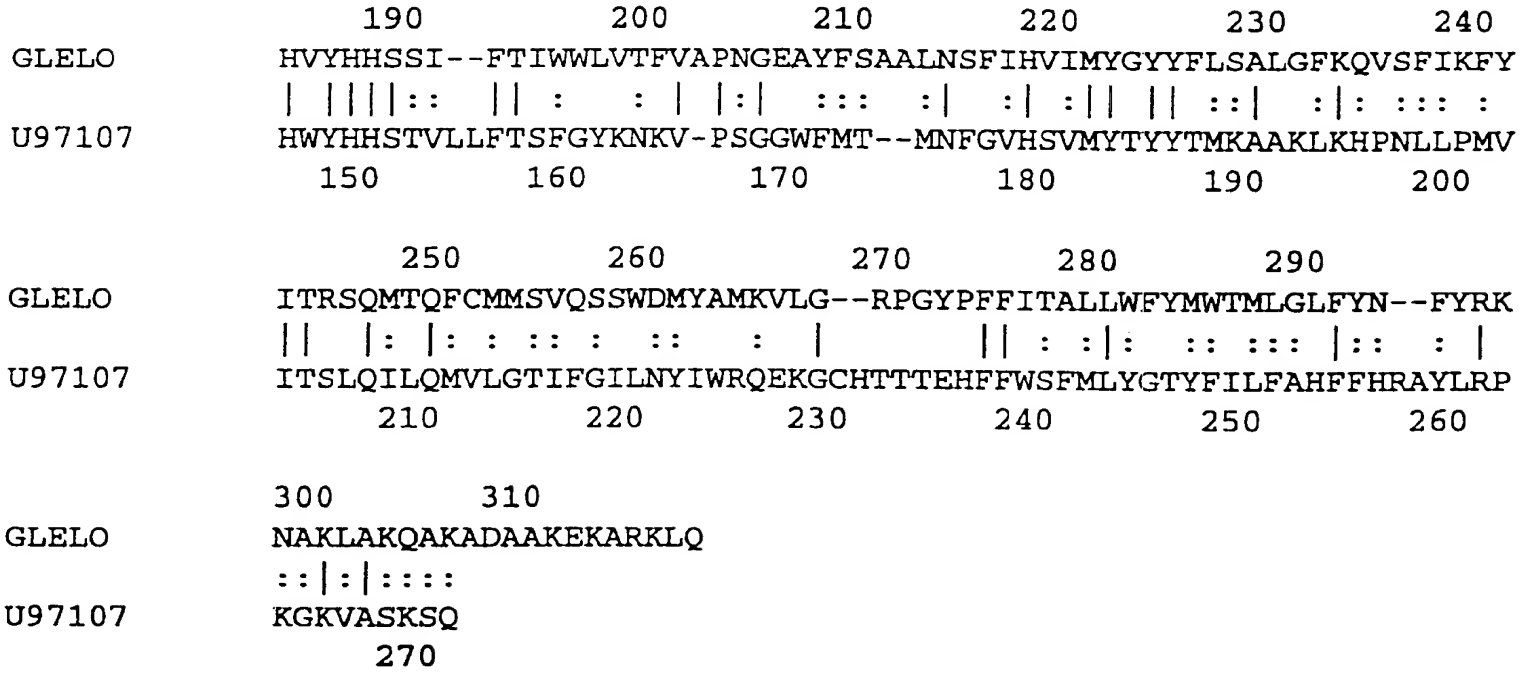
190 200 210 220 230 240
GLELO HVYHHSSI--FTIWWLVTFVAPNGEAYFSAALNSFIHVIMYGYYFLSALGFKQVSFIKFY
U97107 HWYHHSTVLLFTSFGYKNKV-PSGGWFMT--MNFGVHSVMYTYYTMKAAKLKHPNLLPMV
150 160 170 180 190 200
250 260 270 280 290
GLELO ITRSQMTQFCMMSVQSSWDMYAMKVLG--RPGYPFFITALLWFYMWTMLGLFYN--FYRK
U97107 ITSLQILQMVLGTIFGILNYIWRQEKGCHTTTEHFFWSFMLYGTYFILFAHFFHRAYLRP
210 220 230 240 250 260
300 310
GLELO NAKLAKQAKADAAKEKARKLQ
U97107 KGKVASKSQ
270

FIG.38B

```
                    60         70         80         90        100        110
GLELO          TRGFLVAVESPLARELPLMNPFHVLLIVLAYLVTVFVGMQIMKNFERFEVKTFSLLHNFC
                                                 |:|:||    :|:| : |::     : ||
U68749         ATHGPKNFPDAEGRKFFADHFDVTIQASILYMVVVFGTKWFMRNRQPFQLTIPLNIWNFI
(F56H11.4)          30         40         50         60         70         80

                   120        130             140        150        160
GLELO          LVSISAYMCGGILYEAYQ--ANYGL---FENAADHTFKGLPMAKMIWLFYFSKIMEFVDT
               |:::|      :  | :   || |:   : :: | | ||   :  :|||: ||::|:|||
U68749         LAAFSIAGAVKMTPEFFGTIANKGIVASYCKVFDFT-KG-ENGYWVWLFMASKLFELVDT
(F56H11.4)          90        100        110        120        130        140

               170        180        190        200        210        220
GLELO          MIMVLKKNNRQISFLHVYHHSSIFTIWWLVTFVAPNGEAYFSAALNSFIHVIMYGYYFLS
               :::||:|  | : ||| |||   :   |    ::| |   ::  ||  :|::||:||||
U68749         IFLVLRK--RPLMFLHWYHHILTMIYAWYSHPLTP-GFNRYGIYLNFVVHAFMYSYYFLR
(F56H11.4)             150        160        170        180        190

               230        240        250        260        270        280
GLELO          ALGFKQVSFIKFYITRSQMTQFCMMSVQSSWDMYAMKVLGRP-GYPFFITALLWFYMWTM
               :: ::  :||   ||  |::|| :  :  :   | |:  :    :   :  |  |:  |:
U68749         SMKIRVPGFIAQAITSLQIVQFIISCAVLAHLGYLMHFTNANCDFEPSVFKLAVFMDTTY
(F56H11.4)     200        210        220        230        240        250

               290        300        310
GLELO          LGLFYNFYRKNAKLAKQAKADAAKEKARKLQ
               |:|| ||:
U68749         LALFVNFFLQSYVLRGGKDKYKAVPKKKNN
(F56H11.4)     260        270        280
```

FIG.39

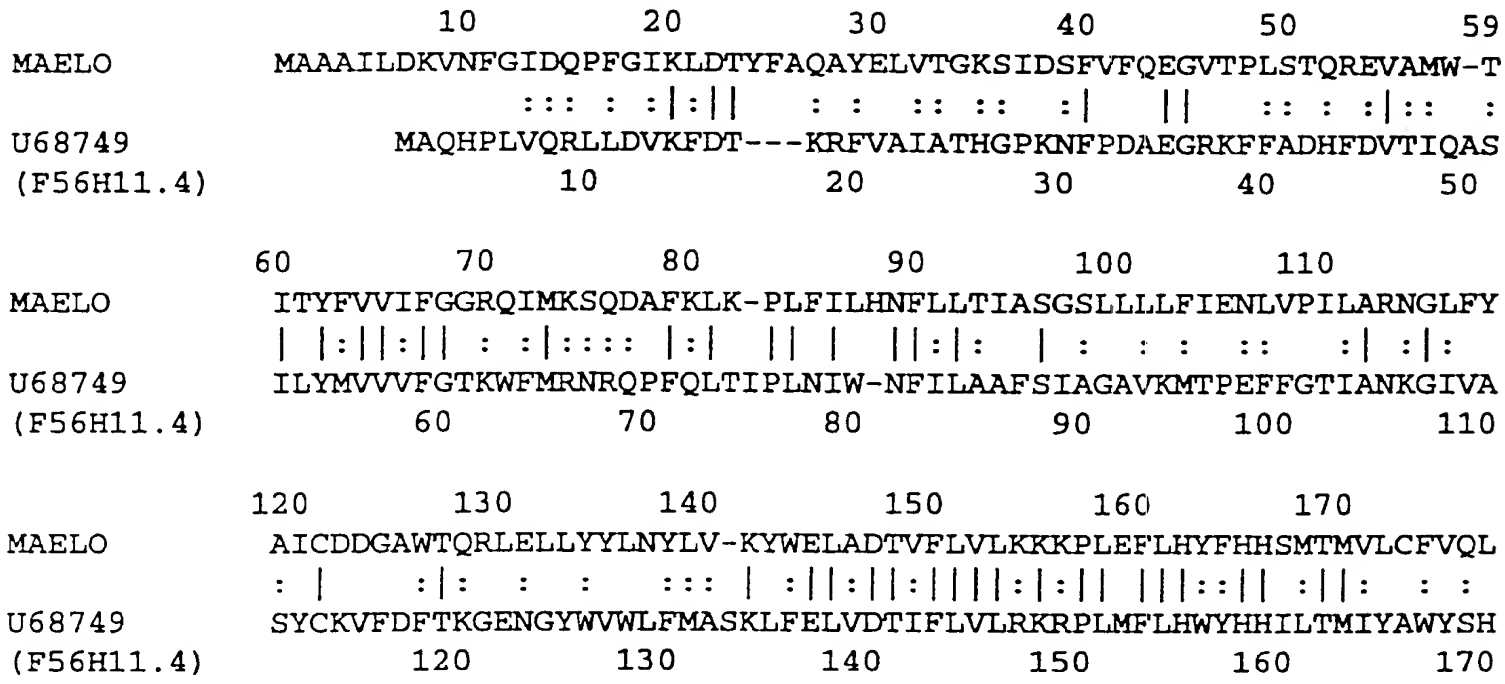
10 20 30 40 50 59
MAELO MAAAILDKVNFGIDQPFGIKLDTYFAQAYELVTGKSIDSFVFQEGVTPLSTQREVAMW-T
U68749 MAQHPLVQRLLDVKFDT---KRFVAIATHGPKNFPDAEGRKFFADHFDVTIQAS
(F56H11.4) 10 20 30 40 50
60 70 80 90 100 110
MAELO ITYFVVIFGGRQIMKSQDAFKLK-PLFILHNFLLTIASGSLLLLFIENLVPILARNGLFY
U68749 ILYMVVVFGTKWFMRNRQPFQLTIPLNIW-NFILAAFSIAGAVKMTPEFFGTIANKGIVA
(F56H11.4) 60 70 80 90 100 110
120 130 140 150 160 170
MAELO AICDDGAWTQRLELLYYLNYLV-KYWELADTVFLVLKKKPLEFLHYFHHSMTMVLCFVQL
U68749 SYCKVFDFTKGENGYWVWLFMASKLFELVDTIFLVLRKRPLMFLHWYHHILTMIYAWYSH
(F56H11.4) 120 130 140 150 160 170

FIG.40A

```
                180       190         200       210          220       230
MAELO           GGYTSVSWVPITLNLTVHVFMY-YYYMRSAAGVRI--WWKQYLTTLQIVQFVLDLGFIYF
                    : :    | ||::||:||| ||::||   :|:  :  | :|:||||||::: : :
U68749          PLTPGFNRYGIYLNFVVHAFMYSYYFLRSMK-IRVPGFIAQAITSLQIVQFIISCAVLAH
(F56H11.4)             180       190       200         210       220

                    240       250       260       270       280
MAELO           CAYT-YFAFTYFPWAPNVGKCAGTEGAALFGCGLLSSYLLLFINFYRITY-----NAKAK
                 :|  :|: :   : |:| | |      :|   : ::|| ||:||:  :|     : | |
U68749          LGYLMHFTNANCDFEPSVFKLA------VF---MDTTYLALFVNFFLQSYVLRGGKDKYK
(F56H11.4)  230       240       250                260       270       280

               290       300       310
MAELO           AAKERGSNFTPKTVKSGGSPKKPSKSKHI
                |: :: :|
U68749          AVPKKKNN
(F56H11.4)
```

FIG.40B

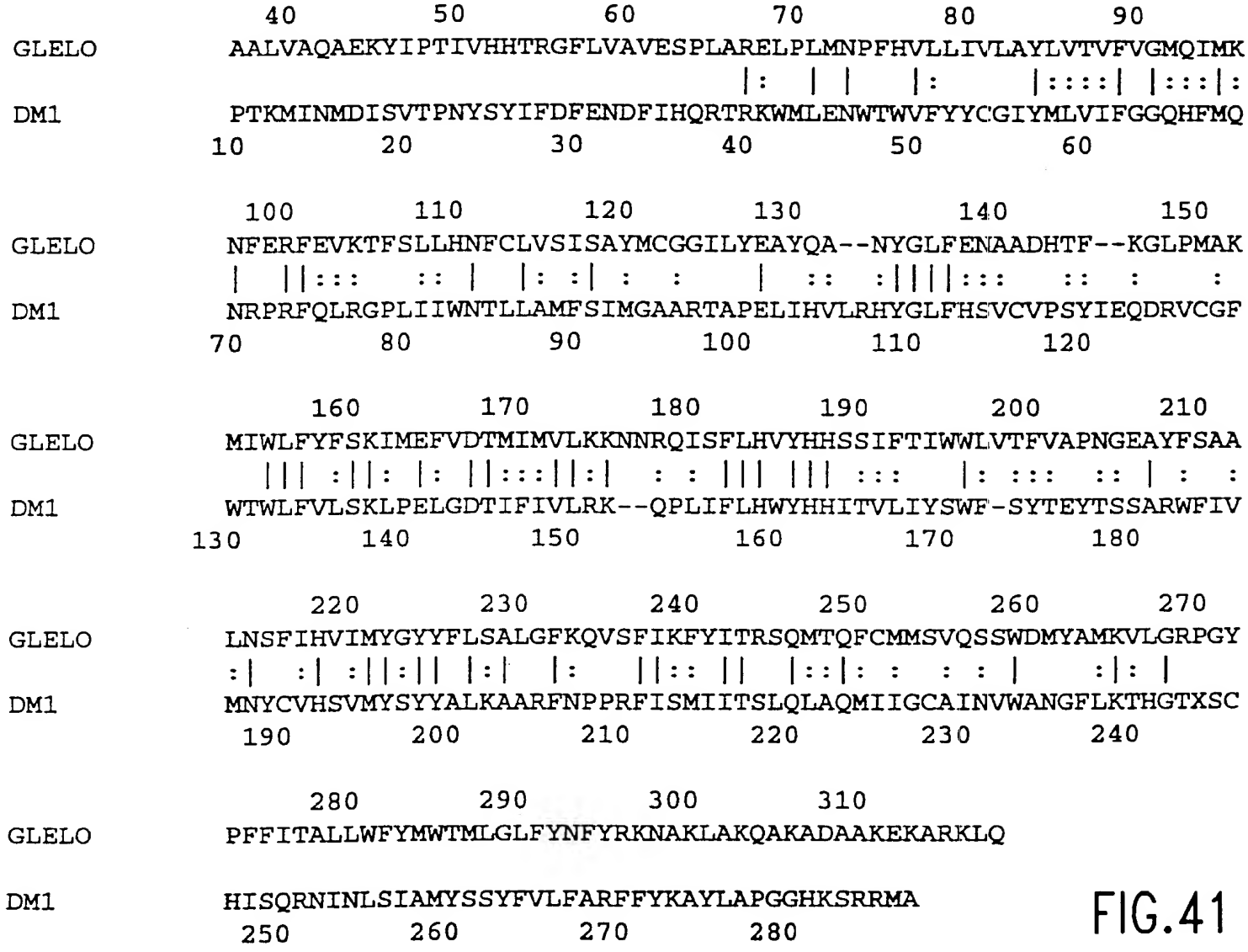
40 50 60 70 80 90
GLELO AALVAQAEKYIPTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYLVTVFVGMQIMK
DM1 PTKMINMDISVTPNYSYIFDFENDFIHQRTRKWMLENWTWVFYYCGIYMLVIFGGQHFMQ
10 20 30 40 50 60
100 110 120 130 140 150
GLELO NFERFEVKTFSLLHNFCLVSISAYMCGGILYEAYQA--NYGLFENAADHTF--KGLPMAK
DM1 NRPRFQLRGPLIIWNTLLAMFSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVCGF
70 80 90 100 110 120
160 170 180 190 200 210
GLELO MIWLFYFSKIMEFVDTMIMVLKKNNRQISFLHVYHHSSIFTIWWLVTFVAPNGEAYFSAA
DM1 WTWLFVLSKLPELGDTIFIVLRK--QPLIFLHWYHHITVLIYSWF-SYTEYTSSARWFIV
130 140 150 160 170 180
220 230 240 250 260 270
GLELO LNSFIHVIMYGYYFLSALGFKQVSFIKFYITRSQMTQFCMMSVQSSWDMYAMKVLGRPGY
DM1 MNYCVHSVMYSYYALKAARFNPPRFISMIITSLQLAQMIIGCAINVWANGFLKTHGTXSC
190 200 210 220 230 240
280 290 300 310
GLELO PFFITALLWFYMWTMLGLFYNFYRKNAKLAKQAKADAAKEKARKLQ
DM1 HISQRNINLSIAMYSSYFVLFARFFYKAYLAPGGHKSRRMA
250 260 270 280

FIG.41

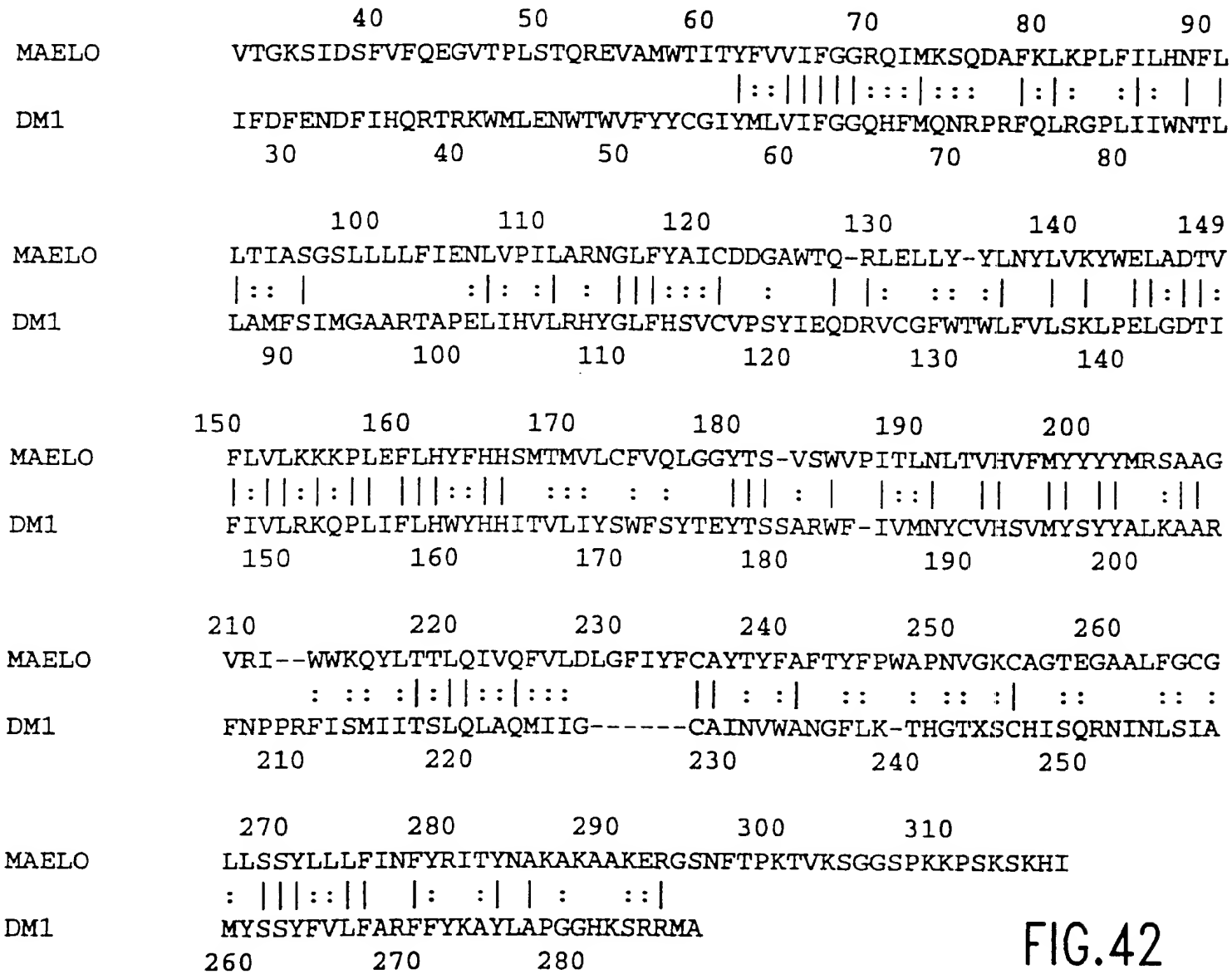
40 50 60 70 80 90
MAELO VTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFILHNFL
DM1 IFDFENDFIHQRTRKWMLENWTWVFYYCGIYMLVIFGGQHFMQNRPRFQLRGPLIIWNTL
30 40 50 60 70 80
100 110 120 130 140 149
MAELO LTIASGSLLLLFIENLVPILARNGLFYAICDDGAWTQ-RLELLY-YLNYLVKYWELADTV
DM1 LAMFSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVCGFWTWLFVLSKLPELGDTI
90 100 110 120 130 140
150 160 170 180 190 200
MAELO FLVLKKKPLEFLHYFHHSMTMVLCFVQLGGYTS-VSWVPITLNLTVHVFMYYYYMRSAAG
DM1 FIVLRKQPLIFLHWYHHITVLIYSWFSYTEYTSSARWF-IVMNYCVHSVMYSYYALKAAR
150 160 170 180 190 200
210 220 230 240 250 260
MAELO VRI--WWKQYLTTLQIVQFVLDLGFIYFCAYTYFAFTYFPWAPNVGKCAGTEGAALFGCG
DM1 FNPPRFISMIITSLQLAQMIIG------CAINVWANGFLK-THGTXSCHISQRNINLSIA
210 220 230 240 250
270 280 290 300 310
MAELO LLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHI
DM1 MYSSYFVLFARFFYKAYLAPGGHKSRRMA
260 270 280

FIG.42

```
  1  ATGGAACATT TTGATGCATC ACTTAGTACC TATTTCAAGG CATTGCTAGG
 51  CCCTCGAGAT ACTAGAGTAA AAGGATGGTT TCTTCTGGAC AATTATATAC
101  CCACATTTAT CTGCTCTGTC ATATATTTAC TAATTGTATG GCTGGGACCA
151  AAATACATGA GGAATAAACA GCCATTCTCT TGCCGGGGGA TTTTAGTGGT
201  GTATAACCTT GGACTCACAC TGCTGTCTCT GTATATGTTC TGTGAGTTAG
251  TAACAGGAGT ATGGGAAGGC AAATACAACT TCTTCTGTCA GGGCACACGC
301  ACCGCAGGAG AATCAGATAT GAAGATTATC CGTGTCCTCT GGTGGTACTA
351  CTTCTCCAAA CTCATAGAAT TTATGGACAC TTTCTTCTTC ATCCTGCGCA
401  AGAACAACCA CCAGATCACG GTCCTGCACG TCTACCACCA TGCCTCGATG
451  CTGAACATCT GGTGGTTTGT GATGAACTGG GTCCCCTGCG GCCACTCTTA
501  TTTTGGTGCC ACACTTAATA GCTTCATCCA CGTCCTCATG TACTCTTACT
551  ATGGTTTGTC GTCAGTCCCT TCCATGCGTC CATACCTCTG GTGGAAGAAG
601  TACATCACTC AGGGGCAGCT GCTTCAGTTT GTGCTGACAA TCATCCAGAC
651  CAGCTGCGGG GTCATCTGGC CGTGCACATT CCCTCTTGGT TGGTTGTATT
701  TCCAGATTGG ATACATGATT TCCCTGATTG CTCTCTTCAC AAACTTCTAC
751  ATTCAGACCT ACAACAAGAA AGGGGCCTCC CGAAGGAAAG ACCACCTGAA
801  GGACCACCAG AATGGGTCCA TGGCTGCTGT GAATGGACAC ACCAACAGCT
851  TTTCACCCCT GGAAAACAAT GTGAAGCCAA GGAAGCTGCG GAAGGATTGA
901  AGTCAAAGAA TTGA
```

FIG.43

```
  1  MEHFDASLST YFKALLGPRD TRVKGWFLLD NYIPTFICSV IYLLIVWLGP
 51  KYMRNKQPFS CRGILVVYNL GLTLLSLYMF CELVTGVWEG KYNFFCQGTR
101  TAGESDMKII RVLWWYYFSK LIEFMDTFFF ILRKNNHQIT VLHVYHHASM
151  LNIWWFVMNW VPCGHSYFGA TLNSFIHVLM YSYYGLSSVP SMRPYLWWKK
201  YITQGQLLQF VLTIIQTSCG VIWPCTFPLG WLYFQIGYMI SLIALFTNFY
251  IQTYNKKGAS RRKDHLKDHQ NGSMAAVNGH TNSFSPLENN VKPRKLRKD*
```

FIG.44

Host (plasmid)	334(pYX242)	334(pRAE-58-A1)	334(pYX242)	334(pRAE-58-A1)
Added substrate	25 µM GLA	25 µM GLA	25 µM AA	25 µM AA
Fatty acid	%total fatty acid	%total fatty acid	%total fatty acid	%total fatty acid
C18:3n-6	4.40	2.71	0.03	0.04
C20:3n-6	0.09	**(50.34%)* 2.75**	0.02	0.02
C20:4n-6			7.84	3.97
C224n-6			ND	**(23.37%)* 1.21**
C16:1n-7	41.11	34.72	41.49	35.07
C18:1n-7	1.85	**11.33**	2.01	**11.57**
C20:1n-7	0.04	**1.48**	0.04	**1.62**
C18:1n-9	15.60	15.66	15.16	14.57
C20:1n-9	0.06	**0.22**	0.06	**0.23**
C18:1n-5	0.11	**0.62**	0.12	**0.58**
Total Lipid	370	969	359	514
*% conversion=product/(substrate+product)				

FIG.45

```
  1  ATGGCTCAGC ATCCGCTCGT TCAACGGCTT CTCGATGTCA AATTCGACAC
 51  GAAACGATTT GTGGCTATTG CTACTCATGG GCCAAAGAAT TTCCCTGACG
101  CAGAAGGTCG CAAGTTCTTT GCTGATCACT TTGATGTTAC TATTCAGGCT
151  TCAATCCTGT ACATGGTCGT TGTGTTCGGA ACAAAATGGT TCATGCGTAA
201  TCGTCAACCA TTCCAATTGA CTATTCCACT CAACATCTGG AATTTCATCC
251  TCGCCGCATT TTCCATCGCA GGAGCTGTCA AAATGACCCC AGAGTTCTTT
301  GGAACCATTG CCAACAAAGG AATTGTCGCA TCCTACTGCA AAGTGTTTGA
351  TTTCACGAAA GGAGAGAATG GATACTGGGT GTGGCTCTTC ATGGCTTCCA
401  AACTTTTCGA ACTTGTTGAC ACCATCTTCT TGGTTCTCCG TAAACGTCCA
451  CTCATGTTCC TTCACTGGTA TCACCATATT CTCACCATGA TCTACGCCTG
501  GTACTCTCAT CCATTGACCC CAGGATTCAA CAGATACGGA ATTTATCTTA
551  ACTTTGTCGT CCACGCCTTC ATGTACTCTT ACTACTTCCT TCGCTCGATG
601  AAGATTCGCG TGCCAGGATT CATCGCCCAA GCTATCACAT CTCTTCAAAT
651  CGTTCAATTC ATCATCTCTT GCGCCGTTCT TGCTCATCTT GGTTATCTCA
701  TGCACTTCAC CAATGCCAAC TGTGATTTCG AGCCATCAGT ATTCAAGCTC
751  GCAGTTTTCA TGGACACAAC ATACTTGGCT CTTTTCGTCA ACTTCTTCCT
801  CCAATCATAT GTTCTCCGCG GAGGAAAAGA CAAGTACAAG GCAGTGCCAA
851  AGAAGAAGAA CAACTAA
```

FIG.46

```
  1  MAQHPLVQRL LDVKFDTKRF VAIATHGPKN FPDAEGRKFF ADHFDVTIQA
 51  SILYMVVVFG TKWFMRNRQP FQLTIPLNIW NFILAAFSIA GAVKMTPEFF
101  GTIANKGIVA SYCKVFDFTK GENGYWVWLF MASKLFELVD TIFLVLRKRP
151  LMFLHWYHHI LTMIYAWYSH PLTPGFNRYG IYLNFVVHAF MYSYYFLRSM
201  KIRVPGFIAQ AITSLQIVQF IISCAVLAHL GYLMHFTNAN CDFEPSVFKL
251  AVFMDTTYLA LFVNFFLQSY VLRGGKDKYK AVPKKKNN
```

FIG.47

Host (plasmid)	334(pYX242)	334(pRET-21)	334(pRET-22)
Added Substrates	50 μM GLA +	50 μM GLA +	50 μM GLA +
	50 μM AA	50 μM AA	50 μM AA
Fatty Acid	%total fatty acid	%total fatty acid	%total fatty acid
C16:0	9.22	12.46	9.9
C16:1	0.09	0.18	0.13
C18:0	1.46	2.41	1.49
C18:1n-9	4.03	4.92	3.91
C18:3n-6	10.02	11.89	8.69
C20:3n-6	**(1.28%)* 0.13**	**(11.1%)* 1.48**	**(19.4%)* 2.09**
C20:4n-6	46.98	28.87	35.25
C22:4n-6	0	0	0
Total lipid (mg)	212	174	187
*% conversion=product/(substrate+product)			

FIG.48

```
  1  ATGAACATGT CAGTGTTGAC TTTACAAGAA TATGAATTCG AAAAGCAGTT
 51  CAACGAGAAT GAAGCCATCC AATGGATGCA GGAAAACTGG AAGAAATCTT
101  TCCTGTTTTC TGCTCTGTAT GCTGCCTTTA TATTCGGTGG TCGGCACCTA
151  ATGAATAAAC GAGCAAAGTT TGAACTGAGG AAGCCATTAG TGCTCTGGTC
201  TCTGACCCTT GCAGTCTTCA GTATATTCGG TGCTCTTCGA ACTGGTGCTT
251  ATATGGTGTA CATTTTGATG ACCAAAGGCC TGAAGCAGTC AGTTTGTGAC
301  CAGGGTTTTT ACAATGGACC TGTCAGCAAA TTCTGGGCTT ATGCATTTGT
351  GCTAAGCAAA GCACCCGAAC TAGGAGATAC AATATTCATT ATTCTGAGGA
401  AGCAGAAGCT GATCTTCCTG CACTGGTATC ACCACATCAC TGTGCTCCTG
451  TACTCTTGGT ACTCCTACAA AGACATGGTT GCCGGGGGAG GTTGGTTCAT
501  GACTATGAAC TATGGCGTGC ACGCCGTGAT GTACTCTTAC TATGCCTTGC
551  GGGCGGCAGG TTTCCGAGTC TCCCGGAAGT TTGCCATGTT CATCACCTTG
601  TCCCAGATCA CTCAGATGCT GATGGGCTGT GTGGTTAACT ACCTGGTCTT
651  CTGCTGGATG CAGCATGACC AGTGTCACTC TCACTTTCAG AACATCTTCT
701  GGTCCTCACT CATGTACCTC AGCTACCTTG TGCTCTTCTG CCATTTCTTC
751  TTTGAGGCCT ACATCGGCAA AATGAGGAAA ACAACGAAAG CTGAATAG
```

FIG.49

```
  1  MNMSVLTLQE YEFEKQFNEN EAIQWMQENW KKSFLFSALY AAFIFGGRHL
 51  MNKRAKFELR KPLVLWSLTL AVFSIFGALR TGAYMVYILM TKGLKQSVCD
101  QGFYNGPVSK FWAYAFVLSK APELGDTIFI ILRKQKLIFL HWYHHITVLL
151  YSWYSYKDMV AGGGWFMTMN YGVHAVMYSY YALRAAGFRV SRKFAMFITL
201  SQITQMLMGC VVNYLVFCWM QHDQCHSHFQ NIFWSSLMYL SYLVLFCHFF
251  FEAYIGKMRK TTKAE*
```

FIG.50

Host	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58
Substrate	GLA	GLA	AA	AA	STA	STA	EPA	EPA	OA	OA	ALA	ALA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
% total lipid												
C18:1n-9	18.75	12.96	16.95	12.76	16.06	14.18	19.55	13.78	29.42	23.06	ND	14.58
C18:1n-7	2.00	18.49	2.30	18.70	1.45	13.26	2.75	13.62	2.50	16.42	1.87	13.76
C18:1n-5	0.29	1.63	0.24	1.61	0.33	0.97	0.32	1.10	0.30	1.64	0.28	1.18
C18:3n-6	4.61	2.02	0.04	0.04	0.02	0.09	0.06	0.05	0.02	0.05	0.01	0.01
C18:3n-3	0.02	0.08	0.02	0.07	0.01	0.03	0.04	0.05	0.02	0.08	14.74	14.08
C18:4n-3	ND	ND	ND	ND	7.01	2.65	ND	ND	ND	ND	ND	ND
C20:1n-9	0.10	0.77	0.11	0.70	0.15	0.55	0.15	0.46	0.27	2.25	0.10	0.57
C20:1n-7	0.08	8.45	0.10	8.06	0.04	3.95	0.14	4.48	0.10	(8.9%)9.35	0.06	3.53
C20:3n-6	0.17	(78.3%)7.29	0.01	0.07	ND	0.04	ND	ND	ND	ND	ND	ND
C20:3n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	0.41	(30.4%) 6.15
C20:4n-6	ND	ND	22.07	8.40	ND	0.07	ND	ND	ND	ND	ND	ND
C20:4n-3	ND	ND	ND	ND	0.25	(79.2%)10.07	ND	ND	ND	ND	ND	ND
C20:5n-3	ND	ND	0.01	ND	0.18	0.08	8.21	2.63	ND	0.02	ND	ND
C22:4n-6	ND	ND	ND	(42.7%)6.26	ND	ND	ND	ND	ND	ND	ND	ND
C22:5n-3	ND	ND	ND	ND	ND	0.18	ND	(71.7%)6.66	ND	ND	ND	ND
Total Lipid	158	104	144	112	324	209	178	94	148	87	243	315

(% conversion) = product/(substrate + product)
ND = not detected

FIG.51

Host	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58
Substrate	GLA	GLA	GLA	GLA	AA	AA	AA	AA	EPA	EPA	EPA	EPA
Concentration	25μM	25μM	100μM	100μM	25μM	25μM	100μM	100μM	25μM	25μM	100μM	100μM
% total lipid												
C18:1n-9	23.82	21.49	18.49	17.41	22.09	19.23	17.45	18.44	24.78	21.28	19.42	18.85
C18:1n-7	2.52	18.35	1.71	11.82	2.54	18.77	1.78	12.67	2.64	19.48	1.79	12.40
C18:1n-5	0.15	1.13	0.10	0.54	0.15	1.23	0.10	0.63	0.15	1.18	0.09	0.62
C18:3n-6	6.10	2.38	23.30	14.46	0.04	0.02	0.04	0.02	0.04	0.02	0.01	0.01
C20:1n-9	0.08	0.83	0.05	0.48	0.10	1.18	0.04	0.56	0.10	1.30	0.06	0.63
C20:1n-7	0.10	5.75	0.07	3.09	0.11	9.49	0.05	3.62	0.10	9.94	0.08	4.07
C20:3n-6	0.15	(62.4%)3.95	0.31	(39.8%)9.56	0.02	ND	ND	0.04	ND	0.02	0.01	0.01
C20:4n-6	ND	ND	0.01	ND	11.76	7.68	28.39	21.02	0.02	0.02	ND	0.01
C20:5n-3	ND	ND	ND	ND	0.03	0.02	0.10	0.07	4.79	2.04	26.47	13.69
C22:4n-6	ND	ND	ND	ND	ND	(27.5%)2.91	0.01	(15.7%)3.90	ND	ND	0.00	ND
C22:5n-3	ND	ND	ND	ND	ND	ND	ND	0.03	0.02	(70.3%)4.82	0.04	(45.7%)11.50
Total Lipid	230	419	590	576	249	332	1014	961	372	390	1323	1065

(% conversion) = product/(substrate + product)
ND = not detected

FIG.52

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58
Substrate	PA	PA	SA	SA	ARA	ARA	BA	BA	PTA	PTA	OA	OA	EA	EA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
% total lipid														
C16:0	24.17	17.23	11.22	7.90	7.74	7.98	7.62	7.11	17.28	11.04	16.06	12.76	14.37	11.98
C16:1n-7	39.83	33.83	30.62	20.56	21.61	19.81	21.34	22.89	50.06	39.43	40.95	30.06	43.34	29.51
C16:1n-5	0.30	0.74	0.29	0.58	0.17	0.47	0.18	0.59	0.38	0.80	0.34	0.68	0.37	0.71
C18:0	1.90	1.50	35.82	38.10	1.12	0.89	1.03	0.88	1.90	1.44	1.82	1.43	1.51	1.23
C18:1n-9	15.36	14.11	11.52	10.88	8.29	10.03	8.09	10.25	14.55	13.86	20.12	21.37	14.12	15.15
C18:1n-7	1.36	11.44	0.90	8.72	0.69	8.51	0.69	8.58	1.30	12.76	1.30	13.79	1.21	12.66
C18:1n-5	0.11	0.78	0.08	0.69	0.08	0.54	0.06	0.61	0.19	0.76	0.10	0.90	0.15	0.84
C20:0	0.15	0.17	0.09	0.12	52.07	41.48	ND	ND	ND	ND	ND	ND	0.17	0.23
C20:1n-9	0.09	0.45	0.05	0.30	0.03	ND	0.06	0.28	0.05	0.38	0.18	0.58	7.47	10.97
C20:1n-7	0.20	2.84	ND	1.52	0.05	1.43	0.14	1.60	0.07	2.76	0.12	2.08	ND	2.30
C22:0	0.43	0.56	0.29	0.22	0.31	0.19	52.91	38.43	ND	ND	ND	ND	ND	0.32
C24:0	0.59	1.39	0.36	0.85	0.45	0.71	0.53	1.14	0.45	1.63	0.66	1.02	0.56	0.79
Total Lipid	297	272	573	542	558	846	585	519	464	295	306	448	309	648

ND = not detected

FIG.53A

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58
Substrate	LA	LA	GLA	GLA	DGLA	DGLA	AA	AA	ADA	ADA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
% total lipid										
C18:1n-9	15.27	16.83	14.85	15.58	13.62	16.24	15.08	15.64	16.18	13.98
C18:1n-7	1.21	13.53	1.22	11.80	1.16	12.63	1.18	11.70	1.30	10.67
C18:1n-5	0.13	0.95	0.20	0.73	0.12	0.72	0.14	0.59	0.12	0.70
C18:2n-6	4.09	4.85	0.09	0.07	0.07	0.04	0.04	0.04	0.03	0.07
C18:3n-6	ND	ND	4.66	2.33	ND	ND	ND	ND	ND	ND
C20:1n-9	0.07	2.60	0.07	0.33	0.07	0.33	0.04	0.27	0.08	0.33
C20:1n-7	0.10	0.18	0.14	1.65	0.08	1.68	0.12	1.58	0.12	1.85
C20:2n-6	ND	(13.2%)0.74	ND	ND	ND	ND	ND	ND	ND	ND
C20:3n-6	ND	ND	ND	(51.4%)2.46	6.37	7.86	ND	0.03	ND	ND
C20:4n-6	ND	ND	ND	ND	ND	0.09	6.49	5.77	ND	ND
C22:4n-6	ND	ND	ND	ND	ND	ND	ND	(27.1%)2.14	10.91	15.57
C24:0	0.59	1.61	0.64	1.12	0.69	0.79	0.52	0.77	0.54	1.26
Total Lipid	333	373	260	392	260	672	553	690	706	440

(% conversion) = product/(substrate + product)
ND = not detected

FIG.53B

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58
Substrate	ALA	ALA	STA	STA	EPA	EPA	DPA	DPA		
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM		
% total lipid										
C18:1n-9	17.21	17.36	16.85	17.71	16.45	16.93	17.08	16.68	18.36	18.77
C18:1n-7	1.29	12.20	1.15	11.38	1.23	11.48	1.33	11.61	1.46	13.72
C18:1n-5	0.14	0.68	0.12	0.57	0.12	0.54	0.12	0.63	0.13	0.79
C18:3n-3	4.42	3.61	ND	0.03	ND	0.03	ND	0.03	ND	0.03
C18:4n-3	ND	0.13	3.04	1.38	ND	0.13	ND	0.13	ND	0.17
C20:1n-9	0.09	0.33	0.11	0.34	0.05	0.31	0.09	0.30	0.13	0.34
C20:1n-7	0.13	1.55	0.05	1.38	0.23	1.89	0.18	1.73	0.15	1.76
C20:3n-3	0.06	(22.2%)1.03	ND	ND	ND	0.11	ND	ND	ND	ND
C20:4n-3	ND	ND	0.06	(61.9%)2.24	ND	ND	ND	ND	ND	ND
C20:5n-3	ND	ND	0.05	0.05	7.43	4.88	ND	ND	0.07	ND
C22:4n-3	ND	ND	ND	0.39	ND	ND	ND	ND	ND	ND
C22:5n-6	ND	ND	ND	ND	ND	ND	0.28	0.41	ND	ND
C22:5n-3	ND	ND	ND	ND	ND	(39.5%)3.19	3.99	5.94	ND	ND
C24:0	0.43	0.73	0.33	0.73	0.45	0.84	0.64	1.07	0.68	0.77
C24:5n-3	ND	ND	ND	ND	ND	0.08	ND	0.06		ND
Total Lipid	696	729	911	710	719	703	602	642	397	684

(% conversion) = product/(substrate + product)
ND = not detected

FIG.53C

```
  1 ATGGAGCAGC TGAAGGCCTT TGATAATGAA GTCAATGCTT TCTTGGACAA
 51 CATGTTTGGA CCACGAGATT CTCGAGTTCG CGGGTGGTTC CTGCTGGACT
101 CTTACCTTCC CACCTTCATC CTCACCATCA CGTACCTGCT CTCGATATGG
151 CTGGGTAACA AGTACATGAA GAACAGGCCT GCTCTGTCTC TCAGGGGCAT
201 CCTCACCTTG TATAACCTCG CAATCACACT TCTTTCTGCG TATATGCTGG
251 TGGAGCTCAT CCTCTCCAGC TGGGAAGGAG GTTACAACTT GCAGTGTCAG
301 AATCTCGACA GTGCAGGAGA AGGTGATGTC CGGGTAGCCA AGGTCTTGTG
351 GTGGTACTAC TTCTCCAAAC TAGTGGAGTT CCTGGACACG ATTTTCTTTG
401 TTCTACGAAA AAAGACCAAT CAGATCACCT TCCTTCATGT CTATCACCAC
451 GCGTCCATGT TCAACATCTG GTGGTGTGTT TTGAACTGGA TACCTTGTGG
501 TCAAAGCTTC TTTGGACCCA CCCTGAACAG CTTTATCCAC ATTCTCATGT
551 ACTCCTACTA CGGCCTGTCT GTGTTCCCGT CCATGCACAA GTACCTTTGG
601 TGGAAGAAGT ACCTCACACA GGCTCAGCTG GTGCAGTTCG TACTCACCAT
651 CACGCACACG CTGAGTGCCG TGGTGAAGCC CTGTGGCTTC CCCTTTGGCT
701 GTCTCATCTT CCAGTCTTCC TATATGATGA CGCTGGTCAT CCTGTTCTTA
751 AACTTCTATA TTCAGACATA CCGGAAAAAG CCAGTGAAGA AAGAGCTGCA
801 AGAGAAAGAA GTGAAGAATG GTTTCCCCAA AGCCCACTTA ATTGTGGCTA
851 ATGGCATGAC GGACAAGAAG GCTCAATAA
```

FIG.54

```
  1 MEQLKAFDNE VNAFLDNMFG PRDSRVRGWF LLDSYLPTFI LTITYLLSIW

 51 LGNKYMKNRP ALSLRGILTL YNLAITLLSA YMLVELILSS WEGGYNLQCQ

101 NLDSAGEGDV RVAKVLWWYY FSKLVEFLDT IFFVLRKKTN QITFLHVYHH

151 ASMFNIWWCV LNWIPCGQSF FGPTLNSFIH ILMYSYYGLS VFPSMHKYLW

201 WKKYLTQAQL VQFVLTITHT LSAVVKPCGF PFGCLIFQSS YMMTLVILFL

251 NFYIQTYRKK PVKKELQEKE VKNGFPKAHL IVANGMTDKK AQ*
```

FIG.55

Host	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	Prae-84	pYX242	pRAE-84
Substrate	GLA	GLA	AA	AA	ADA	ADA	STA	STA	EPA	EPA	DPA	DPA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
% total lipid												
C18:1N-9	15.94	14.16	12.30	15.67	11.77	11.41	14.81	17.92	15.91	16.33	15.04	14.63
C18:1N-7	1.25	1.21	1.10	1.50	1.13	1.18	1.19	1.38	1.33	1.49	1.37	1.38
C18:3N-6	4.53	4.21	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C18:4N-3	ND	ND	ND	ND	ND	ND	2.78	2.70	ND	ND	ND	ND
C20:1N-7	ND	ND	ND	ND	ND	0.32	ND	0.03	ND	0.05	ND	ND
C20:3N-6	0.10	0.37	ND	ND	ND	ND	ND	0.05	ND	ND	ND	ND
C20:4N-6	ND	ND	11.44	5.55	ND	ND	ND	ND	ND	ND	ND	ND
C20:4N-3	ND	ND	ND	ND	ND	ND	ND	(14%)0.44	ND	ND	ND	ND
C20:5N-3	ND	ND	ND	ND	ND	ND	ND	ND	9.68	3.02	ND	ND
C22:4N-6	ND	ND	ND	(10.4%)0.64	20.41	23.61	ND	ND	ND	ND	ND	ND
C22:4N-3	ND	ND	ND	ND	ND	ND	ND	(42.3%)0.33	ND	ND	0.57	0.57
C22:5N-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	(32.7%)1.47	7.87	4.88
C24:4N-6	ND	ND	ND	(62.6%)1.07	ND	(9.2%)2.4	ND	ND	ND	ND	ND	ND
C24:5N-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	(82.8%)7.06	ND	(43.9%)3.82
Total Lipid	208	126	115	189	158	149	124	433	221	271	127	126

(% conversion) = product/(substrate + product)
ND = not detected

FIG.56

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84
Substrate	PA	PA	SA	SA	ARA	ARA	BA	BA	PTA	PTA	OA	OA	EA	EA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
% total lipid														
C16:0	36.30	39.95	7.12	8.31	5.78	4.42	4.17	5.76	18.69	18.85	14.69	18.91	15.25	18.88
C16:1n-7	26.22	23.52	11.77	15.25	10.23	6.29	7.01	10.10	38.48	41.23	20.55	31.48	25.89	40.32
C16:1n-5	0.23	0.28	0.16	0.20	0.13	0.07	0.09	0.13	0.38	0.38	0.26	0.43	0.35	0.41
C18:0	2.26	2.14	64.90	58.73	0.94	1.01	0.64	0.85	2.17	2.29	3.02	2.73	2.71	2.15
C18:1n-9	14.83	11.27	6.35	7.22	5.20	4.33	3.84	5.12	14.25	14.27	18.44	22.20	14.62	16.91
C18:1n-7	1.44	1.36	0.57	0.73	0.54	0.51	0.41	0.56	1.57	1.68	1.53	1.67	1.65	1.84
C18:1n-5	0.10	ND	ND	0.06	ND	ND	ND	0.06	0.17	0.15	ND	0.18	ND	0.16
C20:0	0.59	0.24	0.09	0.08	66.40	74.78	0.10	0.05	0.17	0.17	0.24	0.20	0.33	0.04
C20:1n-9	0.06	0.10	ND	0.04	0.05	0.06	ND	ND	ND	ND	0.25	0.16	13.15	7.07
C20:1n-7	0.07	ND	ND	ND	ND	0.12	ND	ND	ND	ND	0.40	ND	ND	0.04
C22:0	0.45	0.75	0.29	0.30	0.43	0.31	77.35	70.71	0.74	0.80	0.98	0.74	0.83	0.44
C24:0	0.55	1.09	0.38	0.41	0.69	0.62	0.50	0.45	0.94	0.92	1.67	0.96	ND	0.53
Total Lipid	158	104	144	112	324	209	178	94	148	87	243	315	70	529

ND = not detected

FIG.57A

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84
Substrate	LA	LA	GLA	GLA	DGLA	DGLA	AA	AA	ADA	ADA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
	% total lipid									
C18:1n-9	12.30	16.12	15.63	16.28	14.28	13.77	16.21	15.04	15.38	12.94
C18:1n-7	1.34	1.87	1.69	1.90	1.41	1.61	1.61	1.62	1.51	1.47
C18:2n-6	2.67	3.61	0.17	0.20	0.24	0.21	0.09	0.09	0.06	0.14
C18:3n-6	ND	ND	2.03	2.49	ND	ND	ND	ND	ND	ND
C20:3n-6	ND	ND	ND	(14.7%)0.43	10.59	10.73	ND	ND	ND	ND
C20:4n-6	ND	ND	ND	ND	ND	ND	14.03	5.27	ND	ND
C22:4n-6	ND	ND	ND	ND	ND	ND	ND	(8.7%)0.5	11.44	16.60
C24:0	0.79	1.00	1.08	1.16	1.30	0.87	0.87	0.72	0.77	1.18
C24:4n-6	ND	ND	ND	ND	ND	ND	ND	(43.8%)0.39	ND	(7.3%)1.3
C24:5n-6	ND	ND	ND	ND	ND	ND	ND	0.38	ND	ND
Total Lipid	85	87	88	79	107	98	208	212	304	122

*% Conversion=product/(substrate + product)
ND=not detected

FIG.57B

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pXY242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84
Substrate	ALA	ALA	STA	STA	EPA	EPA	DPA	DPA		
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM		
% total lipid										
C18:1n-9	16.69	16.38	18.24	15.95	14.07	15.16	16.05	15.06	17.47	17.15
C18:1n-7	1.37	1.43	1.71	1.40	1.37	1.47	1.67	1.51	1.75	1.73
C18:2n-6	0.08	0.08	0.12	0.04	0.13	0.06	0.11	0.18	0.13	0.15
C18:3n-3	4.47	4.28	ND	ND	ND	ND	ND	ND	ND	ND
C18:4n-3	ND	ND	2.28	2.39	ND	ND	ND	ND	ND	ND
C20:3n-3	(1.3%)0.06	(3.6%)0.16	ND	ND	ND	0.26	ND	ND	ND	0.12
C20:4n-3	ND	ND	ND	(11.1%)0.3	ND	ND	ND	ND	ND	ND
C20:5n-3	ND	0.07	ND	ND	9.97	3.84	ND	ND	ND	ND
C22:4n-3	ND	ND	ND	(43.4%)0.23	ND	ND	ND	ND	ND	ND
C22:5n-6	ND	ND	ND	ND	ND	ND	0.64	0.55	ND	ND
C22:5n-3	ND	ND	ND	ND	ND	(24.0%)1.21	8.79	3.57	ND	ND
C24:0	0.65	0.43	1.41	0.58	1.38	0.78	1.45	1.35	0.89	0.67
C24:5n-3	ND	ND	ND	ND	ND	(73.6%)3.38	ND	(46.4%)3.09	ND	ND
Total Lipid	362	384	173	393	124	280	137	151	190	200

*% conversion = product/(substrate + product)
ND = not detected

FIG.57C

```
  1 ATGGAACATT TCGATGCGTC ACTCAGTACC TATTTCAAGG CCTTCCTGGG
 51 CCCCCGAGAT ACAAGAGTCA AAGGATGGTT CCTCCTGGAC AATTACATCC
101 CTACGTTTGT CTGTTCTGTT ATTTACTTAC TCATTGTATG GCTGGGACCA
151 AAATACATGA AGAACCGGCA GCCGTTCTCT TGCCGAGGCA TCCTGCAGTT
201 GTATAACCTT GGACTCACCC TGCTGTCTCT CTACATGTTC TATGAGTTGG
251 TGACAGGTGT GTGGGAGGGC AAATACAACT TTTTCTGCCA GGGAACACGC
301 AGCGCGGGAG AATCCGATAT GAAGATCATC CGCGTCCTCT GGTGGTACTA
351 CTTCTCCAAA CTCATCGAAT TCATGGACAC CTTTTTCTTC ATCCTTCGCA
401 AGAACAACCA CCAGATCACC GTGCTCCATG TCTACCACCA CGCTACCATG
451 CTCAACATCT GGTGGTTTGT GATGAACTGG GTTCCCTGCG GCCATTCATA
501 TTTTGGTGCG ACACTCAACA GCTTCATCCA TGTCCTCATG TACTCGTACT
551 ATGGTCTGTC CTCCATCCCG TCCATGCGTC CCTACCTCTG GTGGAAAAAG
601 TACATCACTC AAGGGCAGCT GGTCCAGTTT GTGCTGACAA TCATCCAGAC
651 GACCTGCGGG GTCTTCTGGC CATGCTCCTT CCCTCTCGGG TGGCTGTTCT
701 TCCAGATTGG ATACATGATT TCCCTGATTG CTCTCTTCAC AAACTTCTAC
751 ATTCAGACTT ACAACAAGAA AGGGGCCTCT CGGAGGAAAG ACCACCTGAA
801 GGGCCACCAG AACGGGTCTG TGGCCGCCGT CAACGGACAC ACCAACAGCT
851 TCCCTTCCCT GGAAAACAGC GTGAAGCCCA GGAAGCAGCG AAAGGATTGA
```

FIG.58

```
  1  MEHFDASLST YFKAFLGPRD TRVKGWFLLD NYIPTFVCSV IYLLIVWLGP

 51  KYMKNRQPFS CRGILQLYNL GLTLLSLYMF YELVTGVWEG KYNFFCQGTR

101  SAGESDMKII RVLWWYYFSK LIEFMDTFFF ILRKNNHQIT VLHVYHHATM

151  LNIWWFVMNW VPCGHSYFGA TLNSFIHVLM YSYYGLSSIP SMRPYLWWKK

201  YITQGQLVQF VLTIIQTTCG VFWPCSFPLG WLFFQIGYMI SLIALFTNFY

251  IQTYNKKGAS RRKDHLKGHQ NGSVAAVNGH TNSFPSLENS VKPRKQRKD*
```

FIG.59

Host	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-87	pYX242	pRAE-87	pYX242	pRAE-87	pYX242	pRAE-87	pYX242	pRAE-87	pYX242	pRAE-87
Substrate	GLA	GLA	AA	AA	ADA	ADA	STA	STA	EPA	EPA	DPA	DPA
Concentration	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM
% total lipid												
C18:1n-9	15.94	12.05	12.30	12.61	11.77	10.91	14.81	15.52	15.91	16.66	15.04	8.07
C18:1n-7	1.25	8.00	1.10	9.60	1.13	8.87	1.19	8.94	1.33	11.60	1.37	6.90
C18:3n-6	4.53	1.11	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C18:4n-3	ND	ND	ND	0.09	ND	0.14	2.78	0.80	ND	ND	ND	ND
C20:1n-7	ND	0.98	ND	0.91	ND	0.63	ND	0.62	ND	0.94	ND	1.34
C20:3n-6	0.10	(78.7%)4.1	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C20:4n-6	ND	ND	11.44	11.28	ND	ND	ND	ND	ND	ND	ND	ND
C20:4n-3	ND	ND	ND	ND	ND	ND	ND	(81.0%)3.4	ND	ND	ND	ND
C20:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	9.68	4.58	ND	ND
C22:4n-6	ND	ND	ND	(36.0%)6.33	20.41	21.15	ND	ND	ND	ND	ND	ND
C22:4n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	0.57	ND
C22:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	(57.4%)6.18	7.87	17.24
C24:4n-6	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C24:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	(4.2%)0.27	ND	(1.4%)0.25
Total Lipid	208	102	115	177	158	117	124	200	221	199	127	91

(% conversion) = product/(substrate + product)
ND = not detected

FIG.60

Host(plasmid)	334(pYX242)	334(pRET-22)	334(pYX242)	334(pRET-22)	334(pYX242)	334(pRET-22)
Added Substrates	50 mM GLA	50 mM GLA	50 mM AA	50 mM AA	no substrate	no sunstrate
% total lipid						
Fatty Acid						
C16:0	19.8	18.59	13.8	6.23	13.62	13.63
C16:1n-7	20.92	17.74	26.62	13.01	40.1	47.67
C18:0	5.79	4.94	3.62	2	4.86	5.031
C18:1n-7	(3.9%) 0.85	(9.12%) 1.78	(3.5%) 0.97	(12.54%) 1.18	(3.6%) 1.5	(7.53%) 3.88
C18:1n-9	8.46	7.45	10.27	5.36	13.7	16.93
C18:3n-6	*26.62	*22.03	0.03	0.01		
C20:3n-6	**(1.1%)0.3**	**(38.2%)13.61**				
C20:4n-6			*27.36	*65.38		
C22:4n-6						
Total Lipid (μg)	36	42	85	280	55	79
(% conversion) = product/(substrate + product)						
*indicates substrate added						

FIG.61

Host(plasmid)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)
Added Substrate	50μM SA	50μM OA	50μM LA	50μM DGLA	25μM AA	50μM Adrenic
	C18:0	C18:1n-9	C18:2n-6	C20:3n-6	C20:4n-6	C22:4n-6
Fatty Acid	%total lipid					
C16:0	12.9	12.54	15.23	9.1	10.2	3.42
C16:1	37.71	23.83	24.87	16.61	18.375	7.66
C18:0	11.44	4.7	4.49	2.7	2.9	1.23
C18:1n-9	14.03	*16.87	9.54	6.74	6.39	2.99
C18:2n-6			16.87		0.15	0.28
C18:3n-6						
C20:2n-6						0.05
C20:3n-6				*44.34		
C20:4n-6				0.34	*25.78	0.26
C22:4n-6						*75.72
Total Lipid (μg)	63	103	71	110	97	277

*indicates substrate added
(% conversion) = product/(substrate + product)

FIG.62A

Host(plasmid)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)
Added Substrate	50μM ALA	50μM PA	50μM EPA	50μM STA
	C18:3n-3	C18:0	C20:5n-3	C18:4n-3
Fatty Acid	% total lipid			
C16:0	13.91	15.06	16.92	20.08
C16:1	14.74	31.77	23.57	20.17
C18:0	4.06	*4.85	4.94	6.02
C18:1n-9	6.65	13.59	10.46	9.29
C18:3n-3	*38.66			
C18:4n-3				*20.45
C20:4n-3				**(12.57%)2.94**
C20:5n-3				
C22:5n-3			*15.48	
Total Lipid (μg)	80	84	81	60

*indicates substrate added
(% conversion) = product/(substrate + product)

FIG.62B

Host(plasmid)	334(pRET-22+pCGR-4)	334(pYX242+pYES2)
Added Substrate	50μM GLA	50μM GLA
Fatty Acid	% total lipid	
C16:0	15.92	15.07
C16:1n-7	24.97	19.48
C18:0	8.25	6.48
C18:1n-7	3.9	1.61
C18:1n-9	18.48	12.71
C18:3n-6	*7.0	*10.54
C20:0	0	0
C20:3n-6	**(27.81%) 4.36**	**(1.58%) 0.17**
C20:4n-6	**(27.55%) 4.32**	**0**
Total Lipid(μg)	508	168

*indicates substrate added
(% conversion) = product/(substrate + product)

FIG.63A

Host(plasmid)	334(pRET-22+pCGR-4)	334(pYX242+pYES2)
Added Substrate	50μM STA	50μM STA
Fatty Acid	% total lipid	
C16:0	18.74	16.21
C16:1n-7	21.35	26.09
C18:0	6.78	7.57
C18:1n-7	1.97	1.7
C18:1n-9	20.73	22.41
C18:4n-3	*6.05	*13.43
C20:0	0	0.45
C20:4n-3	**(15.88%) 1.68**	**(4.73%) 0.69**
C20:5n-3	**(26.93%) 2.85**	**(3.22%) 0.47**
Total Lipid(μg)	335	161

*indicates substrate added
(% conversion) = product/(substrate + product)

FIG.63B